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[続葉有]

(54) Title: NF-KB ACTIVATING GENE

(54) 発明の名称: NF- κ B 活性化遺伝子

(57) Abstract: A protein having an NF- κ B effect to be used in, for example, diagnosing, treating or preventing diseases in which the excessive activation or inhibition of NF- κ B participate. From a cDNA library prepared from human lung fibroblasts, etc., a cDNA encoding a protein having an effect of activating NF- κ B is cloned by using a plasmid pNF- κ B-Luc and its DNA sequence and an amino acid sequence deduced therefrom are determined. This protein, DNA encoding the same, a recombinant vector containing this DNA and a transformant having this recombinant vector are usable in screening an NF- κ B activation inhibitor or promoter.

(57) 要約:

NF- κ B の過剰な活性化または阻害が関与する疾患の診断、治療または予防等に使用される NF- κ B 作用を有するタンパク質の提供する。

ヒト肺線維芽細胞等から作製した cDNA ライブラリーから、プラスミド pNF- κ B-Luc を用いて、NF- κ B を活性化する作用を有するタンパク質をコードする cDNA をクローニングして、その DNA 配列およびそれより推定されるアミノ酸配列を決定した。同タンパク質、これをコードする DNA、同 DNA を含有する組換えベクターおよび同組換えベクターを含有する形質転換体は、NF- κ B の活性化を阻害または促進する物質のスクリーニングに使用される。

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明 細 書

NF- κ B 活性化遺伝子

技術分野

本発明は、NF- κ B を活性化する作用を有するタンパク質、該タンパク質をコードするDNA、該DNAの取得方法、該DNAを含有する組換えベクター、該組換えベクターを含有する形質転換体ならびに該タンパク質と特異的に反応する抗体に関する。また、本発明は、NF- κ B の過剰な活性化または阻害が関与する疾患の診断、治療または予防を行う際の本発明のタンパク質、DNAまたは抗体の使用に関する。

また本発明は、該タンパク質、DNA、組換えベクターおよび形質転換体を用いて、NF- κ B の活性化を阻害または促進する物質をスクリーニングする方法に関する。

背景技術

転写因子NF- κ B (Nuclear factor kappa B) は、炎症や免疫反応に関与する種々の遺伝子の転写調節において重要な役割を果たしている。NF- κ B は、Relファミリーに属するタンパク質のホモあるいはヘテロ二量体からなり、無刺激の状態では、制御タンパク質であるI κ B (Inhibitor of NF- κ B) と複合体を形成することによりその核移行シグナルが覆い隠され、細胞質内で不活性型として存在する。

細胞にインターロイキン (IL) -1、腫瘍壊死因子 (TNF) - α などのサイトカインの刺激が与えられると、I κ B はIKK (I κ B kinase) によってリン酸化され、ユビキチン化を経て26Sプロテアソームにより分解される。これにより遊離されたNF- κ B は核内に移行し、NF- κ B 結合配列と呼ばれているDNA配列に結合し、その制御下の遺伝子の転写を誘導する。NF- κ B によって発現調節を受けているとされている遺伝子は免疫グロブリン遺伝子の他、IL-1、TNF- α などの炎症性サイトカイン、インターフェロン、細

胞接着因子等が知られており、NF- κ Bはこれらの遺伝子の発現誘導を介して、炎症や免疫応答に関わっている。

NF- κ Bの機能あるいは活性化を阻害することによって、炎症・免疫疾患やその他の疾病、たとえば腫瘍増殖、に関与している多くの因子（タンパク質）の発現を抑制できる可能性があり、自己免疫や炎症を原因・症状とする疾病に対する医薬の有望な標的である〔たとえば、*Clinical Chemistry* 45, 7-17 (1999)、*J. Clin. Pharmacol.* 38, 981-993 (1998)、*Gut* 43, 856-860 (1998)、*The New England Journal of Medicine* 366, 1066-1071 (1997)、*TIPS* 46-50 (1997)、*The FASEB Journal* 9, 899-909 (1995)、*Nature* 395, 225-226 (1998)、*Science* 278, 818-819 (1997)、*Cell* 91, 299-302 (1997)〕。

細胞外からの情報は、何らかのシグナルの形に変えて、細胞膜を通過し細胞質をこえて核に到達し、標的遺伝子の発現を調節して細胞の応答が引き起こされる。そのため、細胞外の刺激からNF- κ Bの活性化に至る細胞内におけるシグナル伝達の仕組みを解明することは、自己免疫疾患や炎症症状を呈する疾患に対する新たな医薬の開発あるいは治療法の開発に非常に重要な手段を提供することとなり、極めて重要な意義を有している。

しかしながら、細胞が一定の刺激を受けてからNF- κ Bの活性化に至るまでのシグナル伝達経路にはプロテインキナーゼなどの各種伝達分子に関わる多くのステップの存在が考えられ、従って、より効率的な創薬研究のためには、主要な役割を果たす伝達分子を明らかにした上でそれらに焦点をしばった新しい薬物スクリーニング方法を確立することが望まれる。しかし、NF- κ Bの活性化のメカニズムは上記IKK、ユビキチン化酵素、26Sプロテアソームの他、TNF receptor associated factor 2 (TRAF2) や NF- κ B inducing kinase (NIK) などの幾つかのシグナル伝達分子が同定され、少しずつ解明されつつあるものの、いまだ不明な点が多く、新たなシグナル伝達分子の同定とより進んだNF- κ B活性化メカニズムの

解明が望まれていた。

発明の開示

本発明の課題は、上記のように有用なNF- κ Bを直接的、あるいは間接的に活性化作用を有する新規な遺伝子、タンパク質を見出し、これを医薬、診断薬、医療の分野で利用する方法を提供することにある。即ち、NF- κ Bを活性化作用を有する新規タンパク質、該タンパク質をコードするDNA、該DNAを含有する組換えベクター、該組換えベクターを含有する形質転換体、該タンパク質の製造方法、該タンパク質またはその部分ペプチドに対する抗体、該抗体の製造方法を提供する。

また、本発明は、該タンパク質、DNA、組換えベクターおよび形質転換体を用いて、NF- κ Bの活性化を阻害または促進する物質をスクリーニングする方法、該スクリーニング用キット、該スクリーニング方法もしくはスクリーニング用キットを用いて得られるNF- κ Bの活性化を阻害または促進する物質、該物質の製造方法、NF- κ Bの活性化を阻害または促進する物質を含有している医薬などを提供する。

近年、生体内で発現している遺伝子を解析する手段として、cDNAの配列をランダムに解析する研究が活発に行われており、このようにして得られたcDNAの断片配列がEST (Expressed Sequence Tag、たとえば<http://www.ncbi.nlm.nih.gov/dbEST>)として、データベースに登録され公開されている。しかし、ESTは配列情報のみであり、その機能を推定することは困難である。また、ESTはUniGene (<http://www.ncbi.nlm.nih.gov/UniGene>)により整備され、これまでに約92000クラスターに登録されている。しかし、その多くは5'端ヌクレオチド配列を欠損しており、タンパク質翻訳開始部位を含まない。そのため、mRNAのコード領域の決定を前提とするタンパク質の機能解析、プロモーターの解析による遺伝子発現制御の理解といった遺伝子機能の解析に直結しているとはいえない。

一方、遺伝子の産物、すなわちタンパク質の機能を解明する方法の一つに、動物細胞を用いた一過性発現クローニング法がある (たとえば、実験医学別冊 遺

伝子工学ハンドブック)。この方法は、動物細胞発現ベクターを用いて作製した cDNA ライブラリーを、動物細胞にトランスフェクションすることで機能的なタンパク質を直接発現させ、このタンパク質が細胞に及ぼす生物活性を指標として cDNA を同定、クローニングする方法である。この方法では、目的とするタンパク質産物に関する化学的情報（アミノ酸配列や分子量）をあらかじめ必要とせず、細胞内や培養液中に発現しているタンパク質の特異的生物活性を検出して cDNA クローンの同定を行うことができる。

この発現クローニングを効率良く行なうためには、cDNA ライブラリーの作製方法を工夫する必要がある。なぜなら、従来より汎用されている cDNA ライブラリー作製方法には幾つかの方法があるが（たとえば Gubler-Hoffman の方法: Gene 25 (1983) オカヤマ-バーグの方法: Mol. Cell. Biol. 2 (1982))、これらの方法によって作製された cDNA は、そのほとんどが 5' 末端ヌクレオチド配列を欠損したものであり、完全長（mRNA の全ヌクレオチド配列を含む）であることは稀であるからである。その理由は、mRNA から cDNA を作るのに使用する逆転写酵素が、完全長の cDNA を作る効率が必ずしも高くないからである。

さらに、遺伝子の機能解析を試みるに際しては、完全長 cDNA をクローニングし、そこからタンパク質を発現させることが必須の要件である。従って、全体のクローンの中で、完全長のものの割合が高いライブラリーを作製することが、発現クローニングを効率良く行なうために必要であった。

本発明者らは、上記課題を解決するために鋭意研究を重ねた結果、オリゴキャッピング法を用いて完全長 cDNA ライブラリーを作製し、293-EBNA 細胞を用いた発現クローニング法による遺伝子機能アッセイ系を完成し、該アッセイ系により NF- κ B を活性化する作用を有するタンパク質をコードする新規 DNA (cDNA) を単離することに成功した。この新規 DNA は、293-EBNA 細胞内で発現させることにより NF- κ B の活性化を誘発した。この結果は、この新規 DNA が NF- κ B の活性化に関与するシグナル伝達分子であることを示しており、本発明を完成するに至った。

すなわち、本発明は

(1) 以下の(a)または(b)の精製されたタンパク質。

(a) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質。

(b) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかにおいて1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- κ Bを活性化作用を有するタンパク質。

(2) 上記(1)記載のタンパク質とその全長にわたり少なくとも95%のアミノ酸配列の同一性を有するタンパク質であり、かつNF- κ Bを活性化作用を有する、精製されたタンパク質。

(3) 以下の(a)または(b)のタンパク質をコードするヌクレオチド配列を包含する、単離されたポリヌクレオチド。

(a) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、4

7、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質。

(b) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかにおいて1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- κ Bを活性化する作用を有するタンパク質。

(4) 以下の(a)～(c)のいずれかのポリヌクレオチド配列を含む単離されたポリヌクレオチド。

(a) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、16

7、169、171、173、175、177または179のいずれかで表されるポリヌクレオチド配列。

(b) (a) のポリヌクレオチド配列と相補的なポリヌクレオチド配列を有するポリヌクレオチドとストリンジェントな条件下でハイブリダイズし、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

(c) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかにおいて、1若しくは複数個のヌクレオチド配列が欠失、置換若しくは付加されたポリヌクレオチド配列からなり、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

(5) 上記(3)記載のポリヌクレオチドと全長にわたり少なくとも95%以上の同一性を有し、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

(6) 上記(4)記載のポリヌクレオチドと全長にわたり少なくとも95%以上の同一性を有し、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

(7) 上記(3)～(6)のいずれか1つに記載のポリヌクレオチドによりコードされる精製されたタンパク質。

(8) 上記(3)～(6)のいずれか1つに記載のポリヌクレオチドを含有する組換えベクター。

(9) 上記(8)に記載の組換えベクターを含む形質転換された細胞。

(10) 上記(1)または(2)に記載のタンパク質が膜タンパク質である場

合における、上記（９）記載の細胞の膜。

（１１） （ａ）上記（３）～（６）のいずれか１つに記載の単離されたポリヌクレオチドがコードするタンパク質を発現する条件下で該ポリヌクレオチドを含有する形質転換された細胞を培養し、

（ｂ）培養物からタンパク質を回収する、
ことを含む、タンパク質の製造方法。

（１２） （ａ）個体のゲノムにおける上記（１）、（２）または（７）に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、
および／または

（ｂ）該個体に由来するサンプル中での該タンパク質の発現量を分析する、
ことを含む該個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法。

上記方法において、好ましくは、発現するタンパク質の量が正常の２倍以上の場合、あるいは２分の１以下の場合に病気であると診断する。

（１３） 以下の工程を含むNF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングする方法。

（ａ）NF- κ Bを活性化するタンパク質をコードする遺伝子およびNF- κ Bの活性化に対応した、検出可能シグナルを提供しうる成分を細胞に提供する工程、

（ｂ）該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された細胞を培養する工程、

（ｃ）該形質転換された細胞と１あるいは複数個の候補化合物とを接触させる工程、

（ｄ）検出可能なシグナルを測定する工程、および

（ｅ）該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物として単離もしくは同定する工程。

また、シグナルを正常より２倍以上増加させる化合物を活性化剤化合物として単離または同定し、２分の１以下に減少させる化合物を阻害剤化合物として単離または同定することが好ましい。

（１４） 以下の工程を含む、医薬組成物を製造する方法。

- (a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子、および検出可能なシグナルを提供しうる成分を細胞に提供する工程、
- (b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された宿主細胞を培養する工程、
- (c) 該形質転換された宿主細胞と1あるいは複数個の候補化合物とを接触させる工程、
- (d) 検出可能なシグナルを測定する工程、
- (e) 該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物を単離もしくは同定する工程、および
- (f) 単離または同定された化合物を医薬組成物として最適化する工程。

また、本発明においては、シグナルを正常より2倍以上増加させる化合物を活性化剤化合物として単離または同定し、2分の1以下に減少させる化合物を阻害剤化合物として単離または同定することが好ましい。

(15) NF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットであって、

(a) NF- κ Bを活性化するタンパク質をコードする遺伝子、およびNF- κ Bの活性化後、検出可能なシグナルを提供しうる成分により形質転換された細胞、および

(b) 検出可能なシグナルを測定するための試薬を含むキット。

(16) 上記(1)、(2)または(7)に記載のタンパク質に特異的に結合するモノクローナルあるいはポリクローナル抗体。

(17) 上記(1)、(2)または(7)に記載のタンパク質を抗原あるいはエピトープ含有フラグメントとして非ヒト動物に投与することからなる、上記(1)、

(2)または(7)に記載のタンパク質に特異的に結合するモノクローナルまたはポリクローナル抗体の製造方法。

(18) NF- κ Bの活性化タンパク質の発現を阻害する、上記(3)～(6)のいずれか1つに記載のポリヌクレオチドに相補的なアンチセンスオリゴヌクレオチド。

(19) 上記(1)、(2)または(7)記載のタンパク質をコードするRNAの開裂により、NF- κ Bの活性化を阻害するリボザイム。

(20) 炎症、自己免疫疾患、感染症、癌および骨疾患からなる群から選択される疾患の治療に有効な量の上記(13)記載の方法でスクリーニングされた化合物および／または上記(16)記載のモノクローナルまたはポリクローナル抗体および／または上記(18)記載のアンチセンスオリゴヌクレオチドおよび／または上記(19)記載のリボザイムを個体に投与することを含む疾患の治療法。

(21) NF- κ Bの活性化を阻害または活性化するものとして上記(14)に記載の方法により製造された医薬組成物。

(22) 炎症、自己免疫疾患、癌、感染症、骨疾患、AIDS、神経変性疾患、または虚血性障害の治療のための上記(21)記載の医薬組成物。

(23) NF- κ Bに関連する疾患を患っている患者に上記(14)記載の方法により製造された医薬組成物を投与することからなる炎症、自己免疫疾患、癌疾患、感染症、骨疾患、AIDS、神経変性疾患、または虚血性障害を治療する方法。

(24) 上記(16)記載のモノクローナルまたはポリクローナル抗体を有効成分として含有する医薬組成物。

(25) 上記(18)記載のアンチセンスオリゴヌクレオチドを有効成分として含有する医薬組成物。

(26) 対象疾患が炎症、自己免疫疾患、感染症、癌疾患、骨疾患、AIDS、神経変性疾患および虚血性障害からなる群から選択される、上記(24)または(25)に記載の医薬組成物。

(27) 機能を有する新規遺伝子の取得方法であり、少なくとも以下の工程を含む方法。

- (a) オリゴキャッピング法を用いて完全長cDNAライブラリーを作製し、
- (b) 完全長cDNAおよび該機能を有するタンパク質の存在を示すシグナルを発する因子を含有するプラスミドを細胞中にコトランスフェクションし、さらに
- (c) シグナルを発するプラスミドを選択する。

尚、本発明における機能を有する新規遺伝子とは、例えば生物活性を持つタン

パク質をコードする核酸分子が挙げられる。

(28) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177および179で表されるヌクレオチド配列のうち少なくとも1以上を含むデータセットおよび／または配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178および180で表されるアミノ酸配列のうち少なくとも1以上を含むデータセットを保存したコンピュータ読み込み可能媒体。

(29) 上記(28)に記載の媒体上のデータと他のヌクレオチド配列および／または他のアミノ酸配列のデータを比較して他のポリヌクレオチド配列および／またはアミノ酸配列との同一性の算出を行う方法。

(30) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、11

4、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質。

(31) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質。

本明細書は本願の優先権の基礎である日本国特許出願 2000-402288 号、2001-088912 号及び 2001-254018 号、並びに、米国仮出願 60/258,315 号、60/278,640 号及び 60/314,385 号の明細書及び／または図面に記載される内容を包含する。

図面の簡単な説明

図1は、実施例3配列番号5のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。図中で横軸は、MG-132濃度、縦軸は、MG-132無添加(0 μ M)条件での相対ルシフェラーゼ活性値を100%とした相対値を示す(各濃度での相対ルシフェラーゼ活性値をMG-132無添加条件での相対ルシフェラーゼ活性で割ってパーセント表示した)。

図 2 は、実施例 3 配列番号 9 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 3 は、実施例 3 配列番号 17 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 4 は、実施例 3 配列番号 21 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 5 は、実施例 3 配列番号 35 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 6 は、実施例 3 配列番号 37 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 7 は、実施例 3 配列番号 41 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 8 は、実施例 3 配列番号 53 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 9 は、実施例 3 配列番号 57 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 10 は、実施例 3 配列番号 63 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 11 は、実施例 3 配列番号 67 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 12 は、実施例 3 配列番号 71 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 13 は、実施例 3 配列番号 75 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 14 は、実施例 3 配列番号 81 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 15 は、実施例 3 配列番号 87 のプロテアソーム阻害剤 MG-132 による NF- κ B のレポーター活性抑制を示す図である。

図 16 は、実施例 3 配列番号 91 のプロテアソーム阻害剤 MG-132 による

NF- κ Bのレポーター活性抑制を示す図である。

図17は、実施例3配列番号93のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図18は、実施例3配列番号97のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図19は、実施例3配列番号121のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図20は、実施例3配列番号123のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図21は、実施例3配列番号129のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図22は、実施例3配列番号154のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図23は、実施例3配列番号158のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図24は、実施例3配列番号162のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図25は、実施例3配列番号168のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図26は、実施例3配列番号170のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図27は、実施例3配列番号172のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図28は、実施例3配列番号176のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

図29は、実施例3配列番号178のプロテアソーム阻害剤MG-132によるNF- κ Bのレポーター活性抑制を示す図である。

配列表の説明

配列番号 181 はプライマーである。

配列番号 182 はプライマーである。

発明を実施するための形態

まず、本発明の基本的特徴を更に明らかにするために、本発明の完成に至る経緯を追いながら、本発明について説明する。NF- κ B を活性化する作用を有する新規遺伝子を取得する目的で、実施例に示すように、以下の実験を実行した。まずヒト正常肺線維芽細胞（三光純薬株式会社より購入）より調製した mRNA より、オリゴキャッピング法によって完全長 cDNA を作製し、該 cDNA をベクター pME18S-FL3 (GenBank Accession AB009864) に組み込んだ完全長 cDNA ライブラリーを作製した。次に、該 cDNA ライブラリーを大腸菌に導入し、1 クローンずつプラスミドを調製した。次に、293-EBNA 細胞（インビトロジェン社）に、ルシフェラーゼをコードする DNA を含有する pNF κ B-Luc レポータープラスミド（STRATAGENE 社）と上記の完全長 cDNA プラスミドとを共導入した。そして、24 時間あるいは 48 時間培養後、ルシフェラーゼ活性を測定し、ルシフェラーゼ活性が対照実験（完全長 cDNA の代わりに、ベクター pME18S-FL3 を入れた細胞）と比べて有意に上昇している（対照実験と比べてルシフェラーゼ活性が 5 倍以上の値を示した）プラスミドを選抜し、該プラスミドにクローニングされている cDNA の全ヌクレオチド配列を決定した。このようにして得られた cDNA によりコードされるタンパク質は、該タンパク質が NF- κ B の活性化に関与するシグナル伝達分子であることを示している。

次に、以下に本発明について詳細に説明する。

本発明における NF- κ B を活性化する作用を有するとは、適切な細胞内に遺伝子を導入し、該遺伝子にコードさせるタンパク質を過剰発現させた時、NF- κ B が直接的あるいは間接的に活性化される（NF- κ B の活性化を誘発する）ことをいう。NF- κ B の活性化は、例えば、NF- κ B 依存レポーター遺伝子を用いたアッセイにより測定できる。アッセイは、該レポーター活性を対照細胞（ベクターのみを導入した細胞）に比し上昇させる作用を有することをいう。レ

ポーター活性の上昇は、好ましくは、1.5倍以上、さらに好ましくは、2倍以上、さらに好ましくは5倍以上である。

レポーター活性は、発現させたいタンパク質をコードするポリヌクレオチド(例えばcDNA)を適切な発現ベクター内にクローニングし、該発現ベクターとNF- κ B依存レポータープラスミドを適切な細胞に共導入(コ・トランスフェクション)し、一定時間培養後、レポーターの活性を測定することにより測定することができる。適切な発現ベクターは当業者にはよく知られており、例えば、pME18S-FL3、pcDNA3.1(Invitrogen社)などが挙げられる。レポーター遺伝子は、当業者がその発現を容易に検出できるものであればよく、例えば、ルシフェラーゼ、クロラムフェニコールアセチルトランスフェラーゼ、 β -ガラクトシダーゼをコードする遺伝子である。ルシフェラーゼをコードする遺伝子を使用することが最も好ましく、NF- κ B依存レポータープラスミドとしては、例えば、pNF- κ B-Luc(STRATAGENE社)が例示される。適切な細胞とは、IL-1あるいはTNF- α などの刺激によりNF- κ Bが活性化される応答を示すような細胞であり、例えば、293-EBNA細胞が挙げられる。細胞培養および細胞への遺伝子導入(トランスフェクション)は、当業者であれば当該技術分野で公知の慣用方法により実施でき最適化できる。

好ましい方法としては、293-EBNA細胞を細胞培養用96穴プレートに 1×10^4 cells/wellの細胞数となるように、5% FBS (Fetal Bovine Serum) 存在下のDMEM (Dulbecco's Modified Eagle Medium) 培地にまき、5% CO₂存在下、37℃で24時間培養した後、FuGENE 6 (Roche社)を用いて、pNF- κ B-Lucレポータープラスミド(STRATAGENE社)と、発現ベクターを1ウェルに共導入する。37℃で24時間培養後、ロングタームルシフェラーゼアッセイシステムピッカジーンLT2.0(東洋インキ社)を用いて、ルシフェラーゼ活性を測定することによりNF- κ Bの活性化を測定する。ルシフェラーゼ活性の測定は、例えば、PerkinElmer社のWallac ARVOTMST 1420 MULTILABEL COUNTERを用いて測定できる。FuGENE 6による遺伝子導入の方法及びピッカ

ジーンLT2.0によるルシフェラーゼ活性測定は、それぞれに添付されているプロトコールに従い実施できる。FuGENE6を用いた96穴プレートでの遺伝子導入の方法は、1ウェルあたり、FuGENE6の量は0.3~0.5 μ lが良く、好ましくは0.3 μ lであり、pNF- κ B-Lucプラスミドの量は50~100ngが良く、好ましくは50ngであり、発現ベクターの量は、50~100ngが良く、好ましくは100ngである。NF- κ Bを活性化する作用を有するとは、該レポーター活性（ルシフェラーゼ活性）を対照実験（空のベクターのみを導入した細胞）に比し、上昇させる作用を有することをいう。レポーター活性の上昇は、好ましくは1.5倍以上、さらに好ましくは、2倍以上、さらに好ましくは5倍以上である。

配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかのアミノ酸配列に関連して、本発明は、以下のタンパク質を提供する。

- (a) 上記アミノ酸配列を含むタンパク質。
- (b) 上記アミノ酸配列の1つを有するペプチド。
- (c) NF- κ Bを活性化し、かつ上記アミノ酸配列において、1以上のアミノ酸の削除、置換または付加を有するタンパク質。

(d) その全長にわたり配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、1

11、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のアミノ酸配列に少なくとも95%、好ましくは97~99%の同一性を有するアミノ酸配列を含むタンパク質。

“同一性”とは、当該技術で知られているとおり、配列を比較することにより決定される、2以上のタンパク質あるいは2以上のポリヌクレオチドの間の関係である。当該技術で“同一性”とは、タンパク質またはポリヌクレオチド配列の間の適合によって、あるいは場合によっては、一続きのそのような配列間の適合によって決定されるような、タンパク質またはポリヌクレオチド配列の間の配列相関性の程度を意味する。“同一性”および“類似性”は、既知の方法により容易に決定できる。同一性を決定する好ましい方法は、試験する配列間で最も長く適合するように設計される。同一性および類似性を決定するための方法は、公に利用可能なプログラムにコードされている。相同性決定には、Altschul らによるBLAST (Basic Local Alignment Search Tool) プログラム (たとえば、Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ., J. Mol. Biol., 215: p403-410 (1990), Altschyl SF, Madden TL, Schaffer AA, Zhang J, Miller W, Lipman DJ., Nucleic Acids Res. 25: p3389-3402 (1997)) を利用し決定することができる。BLAST のようなソフトウェアを用いる場合、デフォルト値を用いるのが好ましい。BLAST 検索に一般的に用いられる主な初期条件は、以下の通りであるが、これに限定されない。

アミノ酸置換行列とは20種類のアミノ酸の各々のペアの類縁性を数値化した行列であり、通常 BLOSUM62 のデフォルトマトリックスが用いられる。このアミノ酸置換行列の理論については Altschul S.F., J. Mol. Biol., 219:555-565 (1991) に、DNA 配列の比較への適用については States D.J., Gish W., Altschul S.F., Methods, 3:66-70 (1991) に示されている。その際の最適なギャップコストは経験的に決定されており、BLOSUM62 の場合は好ましくは、Existence 11、Extension 1 のパラメーターが用いられる。期待値 (EXPECT) とは、データベース配列に対し

てマッチする際の統計的有意性に関する閾値であり、デフォルト値は10である。

一例として、配列番号2のアミノ酸配列に対して例えば95%以上の同一性を有するタンパク質は、そのアミノ酸配列が配列番号2のアミノ酸配列のアミノ酸100個あたり5個までのアミノ酸の変化を含んでよいことを意味する。言い換えれば、対照アミノ酸配列に対して95%以上のアミノ酸配列の同一性を有するタンパク質は、対照配列中の全アミノ酸の5%までの数のアミノ酸が欠失または他のアミノ酸と置換していてもよく、あるいは、対照配列中の全アミノ酸配列のうち5%までの数のアミノ酸が対照配列中に挿入されたものであっても良い。対照配列におけるこれらの変化は、対照アミノ酸配列のアミノ末端またはカルボキシ末端位置に存在していてもよく、あるいはそれらの末端間のいずれかの位置に存在していてもよく、あるいは対照配列内で1個またはそれ以上の一連の群をなしていてもよい。

上記した配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかに記載されたアミノ酸配列からなるタンパク質がNF- κ Bを活性化する作用を有することは、本願明細書実施例に記載の通りである。

配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、1

34、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかのポリヌクレオチドに関連して、本発明は、また以下の単離されたポリヌクレオチドを提供する。

(a) 上記配列に少なくとも95%、好ましくは97-99%の同一性を有するヌクレオチド配列を含むポリヌクレオチド。

(b) 上記配列のポリヌクレオチド。

(c) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかのアミノ酸配列に少なくとも95%、好ましくは97-99%の同一性を有するアミノ酸配列を有するタンパク質をコードするヌクレオチド配列を有するポリヌクレオチド。

上記ヌクレオチド配列に含まれるヌクレオチド配列に同一またはほとんど同一なポリヌクレオチドは、本発明のタンパク質をコードする全長cDNA及びゲノムクローンまたは上記配列に対応する相同性の高い他の遺伝子のcDNAまたはゲノムクローンを単離するためのハイブリダイゼーションプローブとして、または核酸増幅反応のためのプライマーとして使用してもよい。代表的には、これらのヌクレオチド配列は、上記配列に70%同一であり、好ましくは、80%同一であり、より好ましくは90%同一であり、最も好ましくは、95%同一である。プローブまたはプライマーは、一般的には少なくとも15ヌクレオチドを含有し、好ましくは30ヌクレオチドを含有し、50ヌクレオチドを含有してもよい。特に好ましいプローブは、30-50ヌクレオチドを有する。特に好ましいプライマーは、20-25ヌクレオチドを有する。

本発明のポリヌクレオチドは、DNAの形態(たとえば、cDNAおよびクローニングによって得られるか、あるいは合成的に生成されるゲノムDNAを含む)であってもよく、RNA(たとえばmRNA)の形態であってもよい。該ポリヌクレオチドは、二本鎖であっても、一本鎖であってもよい。二本鎖の場合は、二本鎖DNA、二本鎖RNAまたはDNA:RNAのハイブリッドであってもよい。一本鎖の場合は、センス鎖(コード鎖としても知られる)であっても、アンチセンス鎖(非コード鎖としても知られる)であってもよい。

当業者であれば、公知の方法を用いてこのタンパク質中のアミノ酸の置換などを適宜行い、配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかに記載のアミノ酸配列を有するタンパク質と同様にNF- κ Bを活性化する作用を有するタンパク質を作製することが可能である。一つの方法としては、該タンパク質をコードするDNAに対して、慣用の突然変異誘発法を使用する方法がある。別の方法としてはたとえば部位特異的変異法(たとえば宝酒造株式会社のMutagen-Super Express Kmキット)が挙げられる。また、タンパク質のアミノ酸の変異は自然界においても生じうる。このようにアミノ酸の欠失、置換、付加により配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、

131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかのタンパク質に対してアミノ酸配列が変異した変異体であって、NF- κ Bを活性化作用を有するタンパク質及び該タンパク質をコードするDNAも本発明に含まれる。変異の数は、好ましくは10まで、より好ましくは5まで、最も好ましくは3までが好ましい。

アミノ酸置換の例としては、保存的置換が好ましく、具体的には以下のグループ内での置換が挙げられる。(グリシン、アラニン)(バリン、イソロイシン、ロイシン)(アスパラギン酸、グルタミン酸)(アスパラギン、グルタミン)(セリン、トレオニン)(リジン、アルギニン)(フェニルアラニン、チロシン)。

当業者であれば、ハイブリダイゼーション技術などを用いて配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質をコードするDNA(たとえば配列番号2)またはその一部を基に、これと類似性の高いDNAを単離して、該DNAから配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、14

1、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列からなるタンパク質と同様に NF- κ B を活性化する作用を有するタンパク質を得ることも通常行い得ることである。このように上記した配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列のタンパク質と高い同一性を有するタンパク質であって、NF- κ Bを活性化する作用を有するタンパク質も本発明のタンパク質に含まれる。高い同一性とは、上記配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかであらわされるアミノ酸配列の全長にわたり少なくとも90%、好ましくは95%、さらに好ましくは、少なくとも97以上の同一性を有するアミノ酸配列を示す。

本発明のタンパク質としては、ヒトや哺乳動物のあらゆる細胞や組織に由来する天然のタンパク質でもよく、化学合成タンパク質であってもよく、また遺伝子

組換え技術によって得られたタンパク質でもよい。タンパク質は糖鎖やリン酸化などの翻訳後修飾は受けていても受けていなくても良い。

本発明は、上記で示される本発明のタンパク質をコードするポリヌクレオチドである。上記の配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質をコードするヌクレオチド配列としてより具体的には、たとえば配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかで表されるヌクレオチド配列が挙げられる。DNAはcDNAのほか、ゲノムDNA、化学合成DNAも含まれる。遺伝暗号の縮重に従い、遺伝子から生産されるタンパク質のアミノ酸配列を変えることなく配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、

105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質をコードするヌクレオチド配列の少なくとも1つのヌクレオチドを他の種類のヌクレオチドに置換することができる。従って、本発明のDNAはまた、遺伝暗号の縮重に基づく置換によって変換されたヌクレオチド配列も含有する。このようなDNAは、公知の方法により合成することができる。

本発明のDNAは、配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかで表されるヌクレオチド配列からなるDNAとストリンジェントな条件下でハイブリダイズし、かつNF- κ Bを活性化作用を有するタンパク質をコードするDNAも含まれる。ストリンジェントな条件とは、当業者には十分理解できることであり、たとえば、T. Maniatisらの実験操作書 (Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory 1982、1989) に従えば容易に実施できる。

すなわち、ストリンジェントな条件とは、30%ホルムアミドを含むハイブリダイゼーション溶液中 (5×SSC (0.75MのNaCl、75mMのクエン酸三ナトリウム)、5×デンハルト溶液、0.5% SDS、100 μ g/mlの変性せん断サケ精子DNA) で37℃のインキュベーションを一晩行い、その後2

×SSC、0.1% SDS中、室温で10分の洗浄を3回行い、次いで1×SSC、0.1% SDS中、37℃で10分の洗浄を2回行う条件である（低ストリンジエンシー）。より好ましい条件は、40%ホルムアミドを含むハイブリダイゼーション溶液中で42℃のインキュベーションを一晩行い、その後2×SSC、0.1% SDS中、室温で10分の洗浄を3回行い、次いで0.2×SSC、1% SDS中、42℃で10分の洗浄を2回行う条件である（中ストリンジエンシー）。最も好ましい条件は、50%ホルムアミドを含むハイブリダイゼーション溶液中で42℃のインキュベーションを一晩行い、その後2×SSC、0.1% SDS中、室温で10分の洗浄を3回行い、次いで0.2×SSC、0.1% SDS中、50℃で10分の洗浄を2回行う条件である（高ストリンジエンシー）。この際、得られたDNAは、NF- κ Bを活性化作用を有するタンパク質をコードすることが必須である。

本発明は、上記（3）あるいは（4）のポリヌクレオチドのヌクレオチド配列と高い類似性を有し、かつNF- κ Bを活性化作用を有するタンパク質をコードするヌクレオチドを含むポリヌクレオチドを含む。代表的には、これらのヌクレオチド配列は、上記（3）または（4）のポリヌクレオチドのヌクレオチド配列の全長にわたり95%同一であり、より好ましくは97%同一であり、最も好ましくは少なくとも99%同一である。

上記の本発明のDNAは、前述のタンパク質を、組換えDNA技術を用いて製造するのに用いることができる。本発明のDNA及びペプチドは、概略以下のようにして得ることができる。

- (A) 本発明のタンパク質をコードするDNAをクローニングする。
- (B) タンパク質の全コード領域あるいはその一部をコードするDNAを発現用ベクターに組み込んで、組換えベクターを構築する。
- (C) 構築した組換えベクターにより、宿主細胞を形質転換する。
- (D) 得られた細胞を培養し、該タンパク質、またはその類縁体を発現させ、カラムクロマトグラフィーにより精製する。

上記の工程中でDNA、組換え体宿主としての大腸菌等の取り扱いに必要な一般的な操作は、当業者間で通常行われているものであり、たとえば、上記T. M

a n i a t i s らの実験操作書に従えば容易に実施できる。使用する酵素、試薬類も全て市販の製品を用いることができ、特に断らない限り、製品で指定されている使用条件に従えば、完全にそれらの目的を達成することができる。以下に上記 (A) ~ (D) の工程について更に詳しく説明する。

上記 (A) における本発明のタンパク質をコードする DNA のクローニングの手段としては、本願明細書実施例に記載した方法の他に、本発明のヌクレオチド配列 (たとえば配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177 または 179 のいずれか) の一部を有する合成 DNA をプライマーとした PCR 法によって増幅する方法、あるいは、適当なベクターに組み込んだ DNA を本発明のタンパク質の一部あるいは全領域をコードする DNA 断片もしくは合成 DNA を標識したものとのハイブリダイゼーションによって選別すること、などが挙げられる。細胞、組織より全 RNA または mRNA 画分を調製したものを用いて直接 Reverse Transcriptase Polymerase Chain Reaction (RT-PCR 法) によって増幅することもできる。適当なベクターに組み込んだ DNA としては、たとえば市販されている (CLONTECH 社、STRATAGENE 社) ライブラリーを使用することができる。ハイブリダイゼーションの方法は、当業者間で通常行われているものであり、たとえば、上記 T. Maniatis らの実験操作書に従えば容易に実施できる。クローン化された本発明のタンパク質をコードする DNA は目的によりそのまま、または所望により制限酵素で消化したり、リンカーを付加したりして使用することができる。上記のようにして得られる DNA は、配列番号 2、4、6、8、10、12、14、16、

18、20、22、24、26、28、30、32、34、36、38、40、
42、44、46、48、50、52、54、56、58、60、62、64、
66、68、70、72、74、76、78、80、82、84、86、88、
90、92、94、96、98、100、102、104、106、108、1
10、112、114、116、118、120、122、124、126、1
28、130、132、134、136、138、140、142、144、1
46、148、150、151、153、155、157、159、161、1
63、165、167、169、171、173、175、177または179
のいずれかに記載のヌクレオチド配列を有する遺伝子であるか、あるいは前述の
(3)～(6)のポリヌクレオチドであればよい。上記(B)において発現ベク
ターに組み込むDNAは、上述のタンパク質の全長をコードする全長cDNAで
も、DNA断片でも良いし、その一部分を発現する様に構築されたDNA断片で
も良い。

すなわち、本発明は、上記のDNAを含有する組換えベクターである。

本発明のタンパク質の発現ベクターは、たとえば、本発明のタンパク質をコー
ドするDNAから目的とするDNA断片を切り出し、該DNA断片を適当な発現
ベクター中のプロモーターの下流に連結することにより製造することができる。

用いる発現ベクターとしては、複製可能であれば、大腸菌をはじめとする原核
生物由来、酵母由来、真菌由来、昆虫ウイルス由来、脊椎動物ウイルス由来いず
れのベクターでも良いが、宿主として使用する微生物または細胞に適したものを
選択する必要がある。また、発現物に応じて、宿主細胞—発現ベクター系として
は、適切な組み合わせが選択される。

微生物を宿主として使用する場合、これら微生物に適したプラスミドベクター
が組み換え体DNAの複製可能な発現ベクターとして一般に用いられる。

たとえば、大腸菌を形質転換するためのプラスミドベクターとしては、プラス
ミドpBR322やpBR327などを用いることができる。プラスミドベク
ターは通常複製起源、プロモーター、及び組換え体DNAで形質転換した細胞を選
別するのに有用な表現型を組換え体DNAに与えるマーカー遺伝子等を含んでい
る。プロモーターの例としては、 β -ラクタマーゼプロモータ、ラクトースプロ

モーター、トリプトファンプロモーター等が挙げられる。マーカー遺伝子の例としては、アンピシリン耐性遺伝子やテトラサイクリン遺伝子などが挙げられる。適した発現ベクターの例としては、プラスミド pBR322、pBR327 の他に、pUC18、pUC19 等が挙げられる。

酵母で本発明の DNA を発現するためには、複製可能なベクターとして、たとえば YEp24 を用いることができる。プラスミド YEp24 は URA3 遺伝子を含っており、この URA3 遺伝子をマーカー遺伝子として利用することができる。酵母細胞用の発現ベクターのプロモーターの例としては、3-ホスホグリセレートキナーゼ、グリセルアルデヒド-3-ホスフェートデヒドロゲナーゼ、アルコールデヒドロゲナーゼなどの遺伝子プロモーター等が挙げられる。

真菌で本発明の DNA を発現するための発現ベクターに用いられるプロモーター及びターミネーターの例としては、ホスホグリセレートキナーゼ (PGK)、グリセルアルデヒド-3-ホスフェートデヒドロゲナーゼ (GAPD)、アクチン等の遺伝子プロモーター及びターミネーターが挙げられる。適した発現ベクターの例としては、プラスミド pPGACY2、pBSFAHY83 等が挙げられる。

昆虫細胞で本発明の DNA を発現させるための発現ベクターに用いられるプロモーターの例としては、ポリヘドリンプロモーター、P10 プロモーターなどが挙げられる。

動物細胞で本発明の DNA を発現させるための組換えベクターは、一般に遺伝子を制御するための機能配列、たとえば、複製起源、本発明の DNA の上流に位置すべきプロモーター、リボソーム結合部位、ポリアデニル化部位や転写終止配列を含んでいる。本発明の DNA を真核細胞内で発現させるのに用いることができるそのような機能配列はウイルスやウイルス性物質から得ることができる。例えば、SR α プロモーター、SV40 プロモーター、LTR プロモーター、CMV (サイトメガロウイルス) プロモーター、HSV-TK プロモーターなどがあげられる。これらのうち、CMV プロモーター、SR α プロモーターなどを用いるのが好ましい。また、本発明のタンパク質をコードする遺伝子の上流位置に本来存在するプロモーターも、上述の宿主-ベクター系で使用するのに適しているならば使用することができる。複製起源については、外来性の起源、たとえばア

デノウイルス、ポリオーマ、SV40等のウイルス由来の複製起点を用いることができる。また、発現ベクターとして宿主染色体に組み込まれるような性質を有するベクターを用いる場合、宿主染色体の複製起源を利用することができる。適した発現ベクターの例としては、プラスミドpSV-dhfr(ATCC 37146)、pBPV-1(9-1)(ATCC 37111)、pcDNA3.1(INVITROGEN社)、pME18S-FL3等が挙げられる。

本発明は、上記の組換えベクターを含む形質転換された細胞である。本発明の複製可能な組換えベクターで形質転換された微生物または細胞は、前述の通り、組換えベクターに与えられた少なくとも1種の表現型によって形質転換されずに残った親細胞から選別される。表現型は少なくとも1種のマーカー遺伝子を組換えベクターに挿入することによって与えることができる。また複製可能なベクターが本来有しているマーカー遺伝子を利用することもできる。マーカー遺伝子の例としては、たとえば、ネオマイシン耐性などの薬剤耐性遺伝子やジヒドロ葉酸レダクターゼをコードする遺伝子などが挙げられる。

上記(C)において用いる宿主としては、大腸菌をはじめとする原核生物、酵母、真菌等の微生物、及び昆虫や動物等の細胞のいずれでも良いが、用いる発現ベクターに適したものを選択する必要がある。微生物の例としては、エシユリヒア コリ(*Escherichia coli*)の菌株、たとえばE. coli K12株294(ATCC 31446)、E. coli X1776(ATCC 31537)、E. coli C600、E. coli JM109、E. coli B株、あるいはバチラス サブチリス(*Bacillus subtilis*)の如きBacillus属の菌株、あるいはサルモネラ チフィムリウム(*Salmonella typhimurium*)またはセラチア マーゼサンス(*Serratia marcesans*)等の大腸菌以外の腸内菌、あるいはシュードモナス(*Pseudomonas*)属の種々の菌株が挙げられる。酵母としては、たとえば、サッカロミセス セレビスエ(*Saccharomyces cerevisiae*)、シゾサッカロマイセス ポンベ(*Schizosaccharomyces pombe*)、ピキア パストリス(*Pichia pastoris*)などが用いられる。真菌としては、たとえば、アスペルギルス

ニドランズ (*Aspergillus nidulans*)、アクレモニウム ク
リソゲナム (*Acremonium chrysogenum*) (ATCC 11
550) 等が挙げられる。

昆虫細胞としては、たとえば、ウイルスがAcNPVの場合は、夜盗蛾の幼虫
由来株化細胞 (*Spodoptera frugiperda*: Sf細胞)、Tr
ichoplusia niの卵由来のHigh Five™細胞、などが用
いられる。動物細胞の例としては、HEK293細胞、COS-1細胞、COS
-7細胞、HeLa細胞、チャイニーズハムスター (CHO) 細胞等が挙げられ
る。これらの中でも、CHO細胞およびHEK293細胞が好ましい。細胞を
宿主とする場合、用いられる発現ベクターと宿主細胞の組合せは実験の目的によ
り異なるが、その組合せにより、一過的発現、構成的発現の2種類の発現方式が
考えられる。

上記 (C) における微生物及び細胞の形質転換とは、DNAを強制的な方法や、
細胞の貪食能により微生物や細胞に取り込ませ、プラスミド状態あるいは染色体
に組み込まれた状態でDNAの形質を一過的あるいは構成的に発現させることで
ある。当業者であれば公知の方法によって形質転換できる (たとえば実験医学別
冊遺伝子工学ハンドブック)。たとえば動物細胞の場合、DEAE-デキストラン
法、リン酸カルシウム法、エレクトロポレーション法 (電気穿孔法)、リポフェク
ション法などの方法でDNAを細胞に導入することができる。動物細胞を用いて、
本発明のタンパク質を安定に発現させる方法としては、上記の動物細胞に導入さ
れた発現ベクターが染色体に組み込まれた細胞をクローン選択によって選択する
方法がある。具体的には、上記の選択マーカーを指標にして形質転換体を選択す
る。さらに、このように選択マーカーを用いて得られた動物細胞に対して、繰り
返しクローン選択を行なうことにより本発明のタンパク質の高発現能を有する安
定な動物細胞株を得ることができる。また、Dihydrofolate re
ductase (DHFR) 遺伝子を選択マーカーとして用いた場合Metho
trexate (MTX) 濃度を徐々に上げて培養し、耐性株を選択することによ
り、DHFR遺伝子とともに、本発明のタンパク質をコードするDNAを細胞
内で増幅させて、さらに高発現の動物細胞株を得ることもできる。

上記の形質転換された細胞を本発明のタンパク質をコードするDNAが発現可能な条件下で培養し、本発明のタンパク質を生成、蓄積せしめることによって、本発明のタンパク質を製造することができる。すなわち、本発明は、上記（３）～（６）に記載の単離されたポリヌクレオチドを含む形質転換された細胞を、該ポリヌクレオチドによりコードされているタンパク質を発現させる条件下培養し、次いで培養物から該タンパク質を回収することを含む該タンパク質の製造方法である。

上記の形質転換された細胞の培養は、当業者に公知の方法で行なうことができる（たとえばバイオマニュアルシリーズ４、羊土社）。たとえば動物細胞の場合、各種の動物細胞培養法、たとえば、シャーレ培養、マルチトレイ式培養、モジュール培養などの付着培養、または細胞培養用担体（マイクロキャリアー）に付着させるか生産細胞自体を浮遊化させ浮遊培養等の公知の方法により培養を行なえば良い。培地は通常良く用いられる動物細胞用の培地、たとえばD-MEMやRPMI 1640等を用いれば良い。

上記培養物から本発明のタンパク質を分離精製するには、自体公知の分離・精製法を適切に組み合わせて行なうことができる。これらの公知の分離、精製法としては、塩析や溶媒沈殿法などの溶解度を利用する方法、イオン交換クロマトグラフィーなどの荷電の差を利用する方法、透析法、限外ろ過法、ゲルろ過法、およびSDS-ポリアクリルアミドゲル電気泳動法などの主として分子量の差を利用する方法、アフィニティークロマトグラフィーなどの特異的親和性を利用する方法、逆相高速液体クロマトグラフィーなどの疎水性の差を利用する方法、等電点電気泳動法などの等電点の差を利用する方法などが用いられる。たとえば、本発明のタンパク質は、硫酸またはエタノール沈殿、酸抽出、アニオンまたはカチオン交換クロマトグラフィー、ホスフォセルロースクロマトグラフィー、疎水性相互作用クロマトグラフィー、アフィニティークロマトグラフィー、ヒドロキシアパタイトクロマトグラフィーおよびレクチンクロマトグラフィーを含む既知の方法により組換え細胞培養物から回収し、精製することができる。最も好ましくは、高性能液体クロマトグラフィーが精製に使用される。ポリペプチドが細胞内合成、単離または精製の間に変性するときには、活性なコンフォーメーションを再生する

ためにタンパク質をリフォールディングするためのよく知られた技術を使用できる。

本発明のタンパク質を他のタンパク質との融合タンパク質として製造することができる。これらも、本発明に含まれる。この融合タンパク質を発現する際に用いられるベクターとしては、該タンパク質をコードするDNAを組み込むことができ、かつ該融合タンパク質を発現することができるベクターであれば、いかなるベクターでも用いることができる。本発明のペプチドに融合できるタンパク質としては、たとえばグルタチオン-S-トランスフェラーゼ (GST)、ヒスチジン残基の6個の連続配列 ($6 \times \text{His}$) 等が挙げられる。本発明のタンパク質を他の蛋白質と融合した蛋白質として発現させた場合には、融合した蛋白質に親和性をもつ物質を用いたアフィニティークロマトグラフィーを用いて精製することができ、有利である。例えば、GSTとの融合蛋白質として生産した場合は、グルタチオンをリガンドとするアフィニティークロマトグラフィーにより精製することができる。

本発明は、上記(7)のタンパク質の活性を阻害するタンパク質を含む。たとえば、抗体や上記(7)のタンパク質の活性中心等に結合し、活性の発現を妨げる他のタンパク質が挙げられる。

本発明は、前記の本発明のタンパク質あるいはその部分ペプチドに特異的に結合する抗体ならびにそのような抗体の製造方法に関する。抗体は、本発明のタンパク質を認識し得る抗体であれば、ポリクローナル抗体、モノクローナル抗体、ならびにこれらの抗体のフラグメント、一本鎖抗体、ヒト化抗体の何れであってもよい。抗体フラグメントは、公知の技術によって作製することができる。たとえば、該抗体フラグメントには、限定されるものではないが、 $F(a b')$ 2フラグメント、 $F a b'$ フラグメント、 $F a b$ フラグメント及び $F v$ フラグメントが含まれる。たとえば、モノクローナル抗体またはポリクローナル抗体は、上記(1)または(2)に記載のタンパク質を抗原またはエピトープ含有フラグメントとして非ヒト動物に投与することにより得られる。本発明のタンパク質に対する抗体は、本発明のタンパク質あるいはそのペプチドを抗原として用い、自体公知の抗体または抗血清の製造法に従って製造することができる。たとえば実験医学別冊

新遺伝子工学ハンドブック 改訂第3版に記載の方法が挙げられる。

ポリクローナル抗体の場合であれば、たとえば、本発明のタンパク質をウサギなどの動物に本発明のタンパク質あるいはペプチドを注射することにより該タンパク質あるいはペプチドに対する抗体を産生させ、次いで血液を採取し、これを、たとえば硫酸沈殿、イオン交換クロマトグラフィー、あるいは該タンパク質を固定化したアフィニティーカラム等によって精製することで調製することができる。

モノクローナル抗体の場合は、たとえば、本発明のタンパク質をマウスなどの動物に免疫し、同マウスから脾臓を抽出し、これをすりつぶして細胞にし、マウスミエローマ細胞とポリエチレングリコールなどの試薬により融合させ、これによりできた融合細胞（ハイブリドーマ）の中から、本発明のタンパク質に対する抗体を産生するクローンを選択する。次いで、得られたハイブリドーマをマウス腹腔内に移植し、同マウス内より腹水を回収し、得られたモノクローナル抗体を、たとえば硫酸沈殿、イオン交換クロマトグラフィー、あるいは該タンパク質を固定化したアフィニティーカラム等によって精製することで調製することができる。

得られた抗体をヒトに投与する目的で使用する場合は、免疫原性を低下させるために、ヒト型化抗体あるいはヒト抗体を用いることが好ましい。ヒト型化抗体は、トランスジェニックマウスまたは他の哺乳動物を用いて作製することができる。これらのヒト型化抗体のやヒト抗体の一般的概説は、たとえば、M o r r i s s o n, S. L. et al. [Proc. Natl. Acad. Sci. USA, 81: 6851-6855 (1984)], Jones, P. T. et al [Nature 321: 522-525 (1986)], 野口浩 [医学のあゆみ 167: 457-462 (1993)], 松本隆志 [化学と生物 36: 448-456 (1998)] によって供されている。ヒト化キメラ抗体は、マウス抗体のV領域とヒト抗体のC領域を遺伝子組換えにより結合し、作製することができる。ヒト化抗体は、マウスのモノクローナル抗体から相補性決定部位（CDR）以外の領域をヒト抗体由来の配列に置換することによって作製できる。また、免疫系をヒトのものと入れ換えたマウスを用いて、該マウスを免疫して、通常のモノクローナル抗体と同様に直接ヒト抗体を作製することもできる。これらの抗体は、タンパク質を発現するクローンを単離したり同定するのに使用できる。また、こ

これらの抗体は、本発明のタンパク質を細胞抽出液、または本発明のタンパク質を産生する形質転換細胞から精製するのに使用できる。更にこれらの抗体は、細胞や組織中の本発明のタンパク質を検出するELISAやRIA（ラジオイムノアッセイ）、またはウエスタンブロット系の構築に使用できる。このような検出系は、動物、好ましくは、ヒトの組織または血管内流体などの身体サンプル中に存在する本発明のタンパク質の存在量を検出する診断目的に使用することができる。たとえば、これらの抗体は、炎症、自己免疫疾患、感染症（一例としてHIV感染）、骨疾患、癌などの、本発明のタンパク質の（発現）異常に起因するNF- κ Bの望ましくない活性化または抑制によって特徴付けられる疾患の診断に使用できる。疾患の診断の基礎を提供するために、本発明のタンパク質の発現についての通常値、すなわち標準値が確立されなければならないが、これは当業者においては周知の技術である。すなわち、複合体形成のための適切な条件下で、ヒトあるいは動物のどちらでもよいが、正常の被験者から得られた体液あるいは細胞抽出物と、本発明のタンパク質に対する抗体とを結合させ、この抗体-タンパク複合体の量を化学的または物理的手段により検出し、これを既知量の抗原（本発明のタンパク質）を含む標準液を用いて作成した標準曲線を用いて、正常サンプルから得られた標準値を算出する。標準値と本発明のタンパク質が関係する疾患を潜在的に患う被験者からのサンプルから得られた値と比較し、標準値との偏差によって疾病の存在を確認することができる。また、これらの抗体は、本発明のタンパク質の機能を研究する試薬としても用いることができる。

本発明の抗体は精製され得、次いで、たとえば、炎症、自己免疫疾患、感染症（一例としてHIV感染）、癌などの、本発明のタンパク質の（発現）異常に起因するNF- κ Bの望ましくない活性化によって特徴付けられる疾患の患者に投与され得る。すなわち本発明は、上記に記載の抗体を有効成分として含有する医薬、および抗体を用いた治療方法である。これらの医薬は治療的使用のためにさらなる有効成分または不活性成分（たとえば、従来の薬学的に受容可能なキャリアまたは希釈剤（たとえば、免疫原性アジュバント）と、生理学的に無毒の安定化剤および賦形剤とともに組み合わせられ得る。これらの組み合わせは、濾過滅菌され、そして凍結乾燥により投薬バイアル中に、または安定化水性調製物中の貯蔵物と

して投薬形態にされ得る。患者への投与は、たとえば、動脈内注射、静脈内注射、皮下注射などの当業者に公知の方法により行い得る。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。これらの抗体は、本発明のタンパク質で仲介されるNF- κ Bの活性化を阻害し、治療効果を示す。

本発明のDNAは、細胞内シグナリングプロセスに関与する他のタンパク質を単離、同定、クローン化することにも使用できる。たとえば、本発明のタンパク質をコードするDNA配列は、コードされたタンパク質を「バイト (b a i t)」として用いて、cDNAまたはゲノムDNAライブラリーから、本発明のタンパク質に結合できるタンパク質をコードする他の配列「プレイ (p r e y)」を単離し、クローン化する酵母ツーハイブリッドシステム（たとえばNature、340:245-246 (1989)）に用いることができる。同様の方式で、本発明のタンパク質が、他の細胞タンパク質（たとえばNIK, TRAF2）に結合できるかどうかを決定することができる。あるいは別の方法として、本発明のタンパク質の抗体を用いた免疫沈降法（たとえば、実験医学別冊新遺伝子工学ハンドブック）によって、本発明のタンパク質に結合し得るタンパク質を細胞抽出物から単離する方法が挙げられる。さらに別の方法として、上記に記載のように、本発明のタンパク質を他のタンパク質との融合タンパク質として発現させ、融合タンパク質に対する抗体を用いて免疫沈降法を行ない、本発明のタンパク質に結合し得るタンパク質を単離する方法が挙げられる。

診断アッセイは、前述の方法により、NF- κ Bを活性化する機能を持つ(1)、(2)または(7)のタンパク質遺伝子中の変異を検出することにより疾患の診断や該疾患への感受性を決定するための方法を提供する。さらに、このような疾患は、個体に由来するサンプル中のタンパク質またはmRNAレベルの異常な減少または増加を測定することを含む方法によって診断してもよい。発現の減少または増加は、当該技術でRNAレベルでのポリヌクレオチドの定量によく知られた方法、たとえば、RT-PCRなどの核酸増幅法、およびRNase保護法、ノーザンブロット法その他のハイブリダイゼーション法などの方法で測定できる。宿主に由来するサンプル中のタンパク質レベルの測定に使用され得るアッセイ技

術は、当業者によく知られている。そのような方法には、ラジオイムノアッセイ、競合的結合測定法、ウェスタンブロット分析およびE L I S Aアッセイが含まれる。本発明のDNAは、本発明のタンパク質またはそのペプチドフラグメントをコードするDNAまたはmRNAにおける異常を検出するのに使用できる。本発明は、個体における上記(1)、(2)または(7)に記載のタンパク質の発現に関連した疾患または疾患への感受性を診断する方法に関する。該方法は、タンパク質をコードするポリヌクレオチド配列における変異を、測定することを含む。

本発明のDNAは、本発明のDNAを用いることによって、本発明のタンパク質またはその部分ペプチドをコードするDNAまたはmRNAの異常を検出することができるので、たとえば、該DNAまたはmRNAの損傷、突然変異あるいは発現低下や、増加あるいは発現過多などの遺伝子診断に有用である。すなわち本発明は、個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法であって、

(a) 個体のゲノムにおける請求項1、2または7に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および／または

(b) 該個体に由来するサンプル中での該タンパク質の発現量を分析する、ことを含む診断方法であって、好ましくは発現するタンパク質の量が正常の2倍以上あるいは1/2以下の場合に病気であると診断する方法に関する。

上記(a)により、NF- κ Bを活性化する機能を持つ(1)、(2)または(7)のタンパク質をコードするヌクレオチド配列に変異がある場合は、該変異がNF- κ Bの活性化に関連した疾病を引き起こす可能性がある。あるいは、(b)により、被験者における前記(1)、(2)または(7)のタンパク質発現量を測定し正常値を異なる値を示す場合は、NF- κ Bを活性化する作用を持つ本発明の新規タンパク質の発現量異常がNF- κ Bの活性化に関連した疾病の原因である可能性がある。ここで、(a)のNF- κ Bを活性化する機能を持つ(1)、(2)または(7)のタンパク質をコードするヌクレオチド配列の変異の有無を測定する方法としては、それらのタンパク質をコードする遺伝子のヌクレオチド配列の一部をプライマーとして、RT-PCRを行い、その後通常のヌクレオチド配列決定方法によって配列を決定し、変異の有無を検出できる。あるいは、PCR-SS

CP法 (Genomics、5:874-879、1989年、実験医学別冊新遺伝子工学ハンドブック) によっても変異の有無を調べることができる。

また、(b) のタンパク質発現量を調べる方法としては、たとえば、前記(16)に記載の抗体を利用する方法が挙げられる。

また、本発明は、本発明のタンパク質によるNF- κ Bの活性化を阻害または促進する化合物のスクリーニング方法に関する。

このスクリーニング方法は、

(a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子および検出可能なシグナルを提供し得る成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で形質転換された宿主細胞を培養する工程、

(c) 該形質転換された細胞と1あるいは複数個の被検化合物とを接触させる工程、

(d) 検出可能なシグナルを検出する工程、および

(e) 該検出可能なシグナルの測定により活性化剤化合物および/または阻害剤化合物を分離または同定する工程、

を含む。

また、シグナルを正常より2倍以上増加させる化合物を活性化剤化合物として単離または同定し、2分の1以下に減少させる化合物を阻害剤化合物として単離または同定することが好ましい。

検出可能なシグナルを提供し得る成分としては、たとえばレポーター遺伝子が挙げられる。レポーター遺伝子は、テストを行なう転写因子の活性化を直接検出するかわりに用いられるもので、調べたい遺伝子のプロモーターをレポーター遺伝子につなぎ、レポーター遺伝子の産物の活性を測定することによってプロモーターの転写活性の解析を行なうものである(バイオマニュアルシリーズ4、羊土社(1994))。

レポーター遺伝子としては、その発現産物の活性または生産量(mRNAの生産量も含まれる)を当業者が測定可能なものであれば、いかなるペプチド、タンパク質をコードする遺伝子も用いることができる。たとえば、クロラムフェニコ

ールアセチルトランスフェラーゼ、 β -ガラクトシダーゼ、ルシフェラーゼ等の酵素活性を測定することで利用できる。NF- κ Bの活性化を評価するのに用いるレポータープラスミドとしては、NF- κ B認識配列をレポーター遺伝子の upstream に組み込んだものであればよく、たとえば pNF- κ B-Luc (STRATAGENE社) が利用できる。あるいは、Tanaka S. et al. J. Vet. Med. Sci. Vol. 59 (7)、Rothe M. et al. Science Vol. 269 p1424-1427 (1995) に記載の NF- κ B 依存レポータープラスミドが例示される。

宿主細胞としては、NF- κ Bの活性化を検出し得る細胞であればよく、好ましくは、哺乳動物細胞であり、たとえば 293-EBNA細胞が好適に用いられる。形質転換及び培養に関しては、上記に記載の通りである。

NF- κ Bの活性化を阻害または促進する化合物のスクリーニングは、具体的には、たとえば、一定時間培養した形質転換細胞に、被験物質を任意の量添加し、一定時間後の該細胞が発現するレポーター活性を測定し、被験物質を添加しない細胞のレポーター活性と比較することにより、NF- κ Bの活性化を阻害または促進する化合物をスクリーニングすることができる。レポーター活性の測定は、当業者に公知の方法(たとえばバイオマニュアルシリーズ4、羊土社(1994))で行なうことができる。スクリーニングの被検物質には特に制限はなく、低分子化合物、ペプチドなどが挙げられる。被検物質は、人工的に合成したものであっても、天然に存在するものであっても良い。また単一物質でも、混合物でもよい。検出可能なシグナルとしては、上記レポーター遺伝子の他に、NF- κ Bの活性化によって発現が誘導されることが知られている、たとえば IL-1 や TNF- α の mRNA 量あるいはタンパク質量を測定しても良い。mRNA 量の測定は、たとえばノーザンハイブリダイゼーションや RT-PCR 法などが挙げられる。タンパク質量の測定はたとえば抗体を用いる方法が挙げられる。抗体は公知の方法によって作製しても良いし、市販のもの(たとえば和光純薬工業株式会社)を使用することもできる。

また、以下の (a) ~ (f) の工程により医薬組成物を製造することも可能である。

- (a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子および検出可能なシグナルを与えることができる成分を細胞に提供する工程、
- (b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で形質転換された宿主細胞を培養する工程、
- (c) 該形質転換された宿主細胞と1あるいは複数個の化合物とを接触させる工程、
- (d) 検出可能なシグナルを測定する工程、
- (e) 該検出可能なシグナルの測定により活性化剤化合物および/または阻害剤化合物を単離または同定する工程、および
- (f) 単離または同定された化合物を医薬組成物として最適化する工程。

また、本発明においてシグナルを正常より2倍以上増加させる化合物を活性化剤化合物、2分の1以下に減少させる化合物を阻害剤化合物として単離または同定することが好ましい。

本願発明のタンパク質は、以下の工程により、該タンパク質のアゴニスト、アンタゴニストまたは阻害剤を、構造を基礎にして設計する方法に使用してもよい。

- (a) まず、タンパク質の三次元構造を決定する工程、
- (b) アゴニスト、アンタゴニストまたは阻害剤の反応性部位または結合部位と思われる部位の三次元構造を推論する工程、
- (c) 推論した結合部位または反応性部位に結合するかあるいは結合すると予測される候補化合物を合成する工程、および
- (d) 該候補化合物が本当にアゴニスト、アンタゴニストまたは阻害剤であるか否かを試験する工程。

また本発明は、上記スクリーニングによって得られた化合物を含む。しかしながら、本発明のスクリーニング方法は、上記の方法に限定されるものではない。さらに、上記(14)に記載の方法により医薬組成物を製造する方法も含む。

該候補化合物には特に制限はなく、低分子化合物、ペプチドなどが挙げられ、また、人工的に合成したものであっても、天然に存在するものであっても良い。上記スクリーニングによって得られた化合物は、NF- κ Bの活性化を阻害または促進する作用を有しているので、NF- κ Bの望ましくない活性化あるいは不

活性化に起因する疾患を治療または予防するための医薬として有用である。混合物から目的化合物を単離、精製するには、自体公知の方法、例えば濾過、抽出、洗浄、乾燥、濃縮、結晶化、各種クロマトグラフィー等を適宜組み合わせて行うことができる。化合物の塩を取得したい時は、化合物が塩の形で得られる場合にはそのまま精製すれば良く、また遊離の形で得られる場合には、通常の方法により適当な溶媒に溶解または懸濁し、所望の酸または塩基を添加し、塩を形成させて単離精製すれば良い。本発明の方法を用いて得られる化合物またはその塩を医薬組成物として最適化する工程としては、例えば以下のような常法により製剤化する方法が例示される。すなわち活性成分として有効な量の上記化合物またはその薬理的に許容される塩と、薬理的に許容される担体とを混合すれば良い。製剤化は選択された投与様式に適した形態が選ばれる。経口投与に適した組成物としては、錠剤、顆粒剤、カプセル剤、丸剤、および散剤などの固体形態、溶液剤、シロップ剤、エリキシル剤、および懸濁液剤などの液体形態が挙げられる。非経口投与に有用な形態としては、無菌溶液剤、乳剤、および懸濁液剤が挙げられる。上記の担体としては、例えばゼラチン、乳糖、グルコース等の糖類、コーン・小麦・米・とうもろこし澱粉等の澱粉類、ステアリン酸等の脂肪酸、ステアリン酸カルシウム・ステアリン酸マグネシウム等の脂肪酸塩、タルク、植物油、ステアリンアルコール・ベンジルアルコール等のアルコール、ガム、ポリアルキレングリコール等が挙げられる。これらのうち液状担体の例としては、一般に水、生理食塩水、デキストロースまたは類似の糖溶液、エチレングリコール、プロピレングリコール、ポリエチレングリコール等のグリコール類が挙げられる。

本発明は、NF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットである。該キットは、

(a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子およびNF- κ Bの活性化後、その活性化が検出可能なシグナルを提供する成分を含む細胞、

(b) 該検出可能なシグナルを測定するための試薬、から成り、NF- κ Bの活性化を阻害または促進する化合物をスクリーニングするために必要な試薬類を含む。

別の側面において、本発明は、

(a) 配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177 または 179 で表されるヌクレオチド配列を有する本発明のポリヌクレオチド；

(b) (a) のヌクレオチド配列に相補的なヌクレオチド配列；

(c) 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178 または 180 で表されるアミノ酸配列を有する本発明のタンパク質またはそれらの断片；または

(d) (c) の本発明のタンパク質に対する抗体；
を含む診断キットに関する。

少なくとも (a) ~ (d) のいずれかを含むキットは、炎症、自己免疫疾患、感染性疾患（たとえば HIV 感染）および癌などの疾患または該疾患への感受性を診断するのに有用である。

NF- κ B は、炎症、自己免疫疾患、ガン及びウイルス感染などの多種の病理学的状態におけるその関与のため、薬物デザイン及び治療介入のための魅力的な

標的である。多数の実験が、NF- κ B活性が深い生理学的作用を有し得ることを示している(たとえば、Ann. Rheum. Dis. 57, 738-741 (1998), American Journal of Pathology 152, 793-803 (1998), ARTHRITIS & RHEUMATISM 40, 226-236 (1997), Am. J. Respir. Crit. Care Med. 158, 1585-1592 (1998), J. Exp. Med. 188 1739-1750 (1998), Gut 42, 477-484 (1998), The Journal of Immunology 161, 4572-4582 (1998), Nature Medicine 3, 894-899 (1997))。本明細書中に報告するNF- κ Bを活性化する作用を有する新規タンパク質の発見により、異常なNF- κ B機能を制御する新しい方法が提供された。さらなる具体例において、本発明は、NF- κ Bの活性化を阻害するための前記のNF- κ Bを活性化する作用を有するタンパク質の機能を阻害する化合物を用いる方法に関する。また、本発明は、NF- κ Bの活性化を促進するための前記のNF- κ Bを活性化する作用を有するタンパク質の機能を活性化する化合物を用いる方法に関する。上記スクリーニング方法によって得られた、NF- κ Bの活性化を阻害する化合物は、たとえば炎症、自己免疫疾患(慢性関節リウマチ、全身性エリテマトーデス、喘息など)、感染症、骨疾患、移植片拒絶反応などの、NF- κ Bの望ましくない活性化によって特徴つけられる疾患を治療または予防する医薬として有用である。更に、NF- κ Bの活性化が細胞のアポトーシスを抑制することが、最近明らかになりつつある。上記スクリーニング方法によって得られた、NF- κ Bの活性化を阻害する化合物は、アポトーシスを促進する機能を持つ可能性も考えられる。アポトーシスの誘導が治療につながる疾患としては、腫瘍が挙げられる。

また、NF- κ B活性の異常に関連する疾患としては、例えば、AIDS (acquired immunodeficiency syndrome)、神経変性疾患(アルツハイマー病、パーキンソン病、筋萎縮性側索硬化症など)、虚血性障害(心筋梗塞、再灌流障害などにより起こるものなど)、骨髄形成不良症候群(再生不良性貧血など)、皮膚疾患(Toxic epidermal necrolysis など)、増殖性腎炎(IgA腎炎、紫斑病性腎炎、ループス腎炎)、劇症肝炎などが挙げられる。よって、上記スクリーニング方法によって得られた、NF- κ B活性化を阻害する化合物または促進する化合物はこれらの疾患の治療または予防のための医薬として有用である。

更に、本発明のタンパク質をコードする遺伝子は、癌、自己免疫疾患、アレルギー

ギー性疾患、および炎症性応答を初めとする様々な疾患の治療を目的とした遺伝子治療にも有用である。遺伝子治療とは、疾病の治療を目的として、遺伝子または遺伝子を導入した細胞をヒトの体内に投与することを意味する。本発明のタンパク質や該タンパク質をコードする DNA は、診断目的にも使用できる。

本発明のスクリーニング方法を用いて得られる化合物またはその塩を上述の医薬組成物として使用する場合、常套手段に従って実施することができる。たとえば、錠剤、カプセル剤、エリキシル剤、マイクロカプセル剤、無菌性溶液、懸濁液剤などとして行うことができる。このようにして得られる製剤は安全で低毒性であるので、たとえば、ヒトや哺乳動物（たとえば、ラット、ウサギ、ヒツジ、ブタ、ウシ、ネコ、イヌ、サルなど）に対して投与することができる。患者への投与は、たとえば、動脈内注射、静脈内注射、皮下注射など当業者に公知の方法により行う。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。また、該化合物が DNA によりコードされるものであれば、該 DNA を遺伝子治療用ベクターに組み込み、遺伝子治療を行うことも考えられる。投与量、投与方法は、患者の体重や年齢、症状などにより変動するが、当業者であれば適宜選択することが可能である。すなわち本発明は、上記化合物を有効成分として含有する医薬に関する。

さらに、上記化合物は、炎症、自己免疫疾患、ウイルス性疾患、感染症、ガン、骨疾患などの、NF- κ B 活性の異常によって特徴つけられる疾患を治療または予防する医薬として有用である。すなわち本発明は、上記化合物を含む炎症、自己免疫疾患、ウイルス性疾患、感染症、ガン、骨疾患などの医薬に関する。具体的には、例えば、慢性関節リウマチ、変形性関節症、全身性エリテマトーデス、糖尿病、敗血症、喘息、アレルギー性鼻炎、虚血性心疾患、炎症性腸疾患、くも膜下出血、ウイルス肝炎、エイズ、アテローム性動脈硬化症、アトピー性皮膚炎、ウイルス感染症、クローン病、糖尿病、通風、肝炎、多発性硬化症、心筋梗塞、腎炎、骨粗鬆症、アルツハイマー、パーキンソン病、ハンチントン舞踏病、乾癬、筋萎縮性側索硬化症、心筋梗塞、再生不良性貧血などに対する治療及び予防薬として有用である。

さらにまた、本発明は、炎症、自己免疫疾患、ウイルス性疾患、ガン、感染症、

骨疾患などの医薬の製造における上記（１４）記載の方法により製造された医薬組成物の使用も含む。また本発明は、上記（３）～（６）に記載の遺伝子に対するアンチセンスオリゴヌクレオチドである。アンチセンスオリゴヌクレオチドは、標的とした遺伝子配列に対して相補的な配列を持つオリゴヌクレオチドを用いて、タンパク質への翻訳、細胞質への輸送、あるいは全体的な生物活性機能に必要な他の活性等のRNAの機能を阻害することによって、標的遺伝子の発現を抑制することができる。この際、アンチセンスオリゴヌクレオチドとしては、RNAを用いても良いし、DNAを用いても良い。本発明のDNA配列は、本発明のタンパク質をコードする遺伝子から転写されたmRNAとハイブリダイズし得るアンチセンスオリゴヌクレオチドを作製するために使用できる。一般にアンチセンスオリゴヌクレオチドが、その遺伝子の発現に対して抑制的に作用することは公知での事実である（たとえば、細胞工学 Vol. 13 No. 4 (1994)）。本発明のタンパク質をコードする遺伝子に対するアンチセンスコード配列を有するオリゴヌクレオチドは、標準の方法で細胞内に導入することができ、該オリゴヌクレオチドは、本発明のタンパク質をコードする遺伝子のmRNAの翻訳を効果的に遮断して、その発現を遮断して、望ましくない作用が阻害される。

本発明のオリゴヌクレオチドは、天然に見出されるオリゴヌクレオチドの他に、修飾されたものであっても良い〔たとえば、村上&牧野：細胞工学 Vol. 13 No. 4 p 259-266 (1994)、村上章：蛋白質核酸酵素 Vol. 40 No. 10 p 1364-1370 (1995)、竹内恒成ら：実験医学 Vol. 14 No. 4 p 85-95 (1996)〕。従って、オリゴヌクレオチドは変化した糖部分あるいは糖間部分を有していても良い。これらの例は、当該技術分野において使用が知られているホスホチオエート及び他のイオウ含有種である。幾つかの好ましい態様に従えば、オリゴヌクレオチドの少なくとも一つのホスホジエステル結合が、その活性が調節されるべきRNAが位置する細胞の領域に浸透する組成物の能力を高める機能を有する構造により置換される。

このような置換は、ホスホロチオエート結合、ホスホロアミデート結合、メチルホスホネート結合または短鎖アルキルもしくはシクロアルキル構造を含むことが好ましい。オリゴヌクレオチドはまた、少なくとも幾つかの修飾されたヌクレ

オチド型を含んでいても良い。従って、天然に通常見いだされるもの以外のプリン及びピリミジンを使用していても良い。同様に本発明の本質的な意図が実行される限り、ヌクレオチドサブユニットのフラノシル部分を修飾することもできる。このような修飾の例は、2'-O-アルキル-、及び2'-ハロゲン置換ヌクレオチドである。本発明において有用な幾つかの糖部分の2'位の修飾の例は、OH、SH、SCH₃、OCH₃、OCN、またはO(CH₂)_nCH₃（ここでnは1から約10である）、及び同様の特性を有する他の置換基である。全てのこのような類似体は、本発明の遺伝子のmRNAとハイブリダイズしてそのRNAの機能を阻害する機能を果たす限り、本発明に包含される。

本発明のオリゴヌクレオチドは、約3から約50ヌクレオチドを含み、約8から約30ヌクレオチドを含むことが好ましく、約12から約25ヌクレオチドを含むことがさらに好ましい。本発明のオリゴヌクレオチドは、周知の方法である固相合成法により作製することができる。このような合成のための装置は、Applied Biosystemsを含む幾つかの業者により販売されている。ホスホチオエート等の他のオリゴヌクレオチドの製造も当業者に公知の方法で作製できる。

本発明のオリゴヌクレオチドは、本発明の遺伝子から転写されるmRNAとハイブリダイズできるように設計される。与えられた遺伝子の配列に基づいてアンチセンスオリゴヌクレオチドを設計する方法は、当業者であれば容易である〔たとえば、村上および牧野：細胞工学 Vol. 13 No. 4 p 259-266 (1994)、村上章：蛋白質核酸酵素 Vol. 40 No. 10 p 1364-1370 (1995)、竹内恒成ら：実験医学 Vol. 14 No. 4 p 85-95 (1996)〕。最近の研究は、mRNAの5'領域、好ましくは翻訳開始部位を含む領域に設計されたアンチセンスオリゴヌクレオチドが、遺伝子の発現の阻害に最も効果的であることを示唆している。アンチセンスオリゴヌクレオチドの長さは、15から30ヌクレオチドが好ましく、20から25ヌクレオチドがより好ましい。ホモロジー検索で他のmRNAとの相互作用がないこと、オリゴヌクレオチド配列内で二次構造を取らないことを確認しておくことは重要である。設計したアンチセンス分子が機能したかどうかの評価は、適当な細胞を

用いて、該細胞にアンチセンスオリゴヌクレオチドを導入し、当業者には公知の方法で、対象mRNAの量(たとえば、ノーザンブロットまたはRT-PCR法)、あるいは対象タンパク質の量(たとえば、ウエスタンブロットまたは蛍光抗体法)を測定することにより、発現抑制の効果を確認できる。

一方、三重らせん形成(トリプル・ヘリックス技術)は、核内のDNAを標的とした、主に転写の段階での遺伝子発現制御方法である。オリゴヌクレオチドは、主に転写に関与する遺伝子領域に設計され、それにより、転写及び本発明のタンパク質の産生を抑える。これらのRNA、DNA、オリゴヌクレオチドは、公知の合成装置などを用いて製造することができる。

本発明のオリゴヌクレオチドは、標的核酸配列を含む細胞に、たとえばリン酸カルシウム法、リポフェクション法、エレクトロポレーション法、マイクロインジェクション法などのDNAトランスフェクション法、またはウイルスなどの遺伝子導入ベクターの使用を含む遺伝子導入法のいずれを用いて導入してもよい。適切なレトロウイルスベクターを用いてアンチセンスオリゴヌクレオチド発現ベクターを作製し、その後、該発現ベクターを細胞と*in vivo*または*ex vivo*で接触させることにより、標的核酸配列を含む細胞に導入できる。

本発明のDNAは、アンチセンスRNA/DNA技術またはトリプル・ヘリックス技術を用いて、本発明のタンパクを介するNF- κ Bの活性化を阻害するのに使用できる。

本発明のタンパク質をコードする遺伝子のアンチセンスオリゴヌクレオチドは、たとえば炎症、自己免疫疾患、感染症(たとえば、HIV感染症)、ガンなどの、NF- κ Bの望ましくない活性化によって特徴つけられる疾患を治療または予防する医薬として有用である。すなわち、本発明は、上記アンチセンスオリゴヌクレオチドを有効成分として含有する医薬である。また、本発明のアンチセンスオリゴヌクレオチドは、ノーザンハイブリダイゼーション法またはPCR法を用いてそれらの疾病の検出に利用することもできる。

本発明は、NF- κ Bの活性化を阻害するリボザイムも含む。リボザイムは、核酸のヌクレオチド配列を認識して、核酸を切断する活性を持つRNAである(たとえば、柳川弘志 実験医学バイオサイエンス12、RNAのニューエイジ)。リ

ボザイムは、選択された標的RNA、たとえば本発明のタンパク質をコードするmRNAを開裂するように製造することができる。本発明のタンパク質をコードするDNAのヌクレオチド配列を基に、本発明のタンパク質のmRNAを特異的に切断するリボザイムを設計することができ、かようなリボザイムは本発明のタンパク質のmRNAに対して相補的な配列を有し、該mRNAと相補的結合し、ついで該mRNAが開裂され本発明のタンパク質の発現が減少する（または完全に発現しない）。発現減少のレベルは標的細胞内でのリボザイム発現のレベルに依存している。

よく用いられるリボザイムには、ハンマーヘッド型とヘアピン型の2種類があり、特にハンマーヘッド型リボザイムは切断活性に必要な一次構造や二次構造がよく調べられており、当業者であれば、本発明のタンパク質をコードするDNAのヌクレオチド配列情報のみで容易にリボザイムの設計が可能である〔たとえば、飯田ら：細胞工学 Vol. 16 No. 3, p438-445 (1997)、大川&平比良：実験医学 Vol. 12 No. 12 p83-88(1994)〕。ハンマーヘッドリボザイムは、標的RNAと相補鎖を形成する2ヶ所の認識部位（認識部位Iと認識部位II）と活性部位からなる構造をなし、標的RNAと認識部位で相補対を形成した後、標的RNAのNUXの配列（N：AまたはGまたはCまたはU、X：AまたはCまたはU）の3'末端側で切断することが知られており、特にGUC（あるいはGUA）が一番高い活性を持つことが知られている〔たとえば Koizumi, M ら：Nucl. Acids Res. 17, 7059-7071(1989)、飯田ら：細胞工学 Vol. 16 No. 3, p438-445 (1997)、大川&平比良：実験医学 Vol. 12 No. 12 p83-88(1994)、川崎&多比良：実験医学 Vol. 18 No. 3 p381-386 (2000)〕。

そこでまず、本発明のDNA配列の中からGTC（またはGTA）の配列を探し出し、その前後で数ヌクレオチドから十数ヌクレオチドの相補対をつくることできるようにリボザイムを設計する。設計したリボザイムの適切性の評価は、たとえば、大川&平比良の文献〔実験医学 Vol. 12 No. 12 p83-88(1994)〕に記載の方法によって、作製したリボザイムが、インビトロで標的mRNAを切断できるかどうかを調べることで評価できる。リボザイムの調製は、RNA分子を合成するための当分野で周知の方法により調製する。

別法としては、リボザイムの配列をDNA合成機で合成し、たとえばT7或いはSP6のような適切なRNAポリメラーゼプロモーターを有する多種のベクターに組み込み、インビトロで酵素的にRNAを合成させる方法が挙げられる。これらのリボザイムは、たとえばマイクロインジェクション法などの遺伝子導入方法によって細胞内に導入できる。あるいは別の方法として、リボザイムDNAを適当な発現ベクターに組み込んで、株細胞、細胞或いは組織内に導入する。選択された細胞中にリボザイムを導入するのに、適切なベクターを使用することができ、たとえばプラスミドベクター、動物ウイルス（たとえばレトロウイルス、アデノウイルス、ヘルペスあるいはワクシニアウイルス）ベクターがこれらの目的に通常用いられる。これらのリボザイムは、本発明のタンパク質で仲介されるNF- κ Bの活性化を阻害する作用を有する。

本発明はまた、機能を有する新規遺伝子の取得方法であり、オリゴキャッピング法を用いて完全長cDNAライブラリーを作製する方法および該機能を有するタンパク質の存在を示すシグナル因子を用いる方法からなる取得方法に関する。シグナル因子には、たとえばレポーター遺伝子が挙げられる。

機能を有する遺伝子（cDNA）を多数取得するためには、不完全長のものが多いcDNAライブラリーを用いると効率が悪い。したがって、全体のクローンの中で、完全長のものの割合が高いライブラリーが必要となる。完全長cDNAは遺伝子から出来るmRNAの完全なコピーのことである。オリゴキャッピング法で作製したcDNAライブラリーは、完全長cDNAの割合が50～80%であり、従来の方法で作製されたcDNAライブラリーと比べて、5～10倍の完全長cDNAクローンの濃縮になっている（菅野純夫：月刊 BIO INDUSTRY Vol. 16 No. 11 p19-26）。完全長cDNAは、遺伝子の機能解析においては、タンパク質発現のために必須なクローンであり、完全長cDNAのクローンそのものが活性測定のための材料として極めて重要なものであるため、遺伝子の機能解析を試みるに際して、完全長cDNAのクローニングは必須の要件である。さらにその配列を決定することで、それがコードするタンパク質の一次配列を確定するための重要な情報となると同時に、遺伝子の全エクソンの配列も分かる。すなわち、完全長cDNAは、遺伝子を同定する上で貴重な情報、たとえばタンパク質の一次配

列、エクソン-イントロン構造、mRNAの転写開始点、プロモーターの位置などを決めるための情報をも与える。

オリゴキャッピング法による完全長cDNAライブラリー作製は、たとえば実験医学別冊新遺伝子工学ハンドブック改訂第3版（1999年）に記載の方法に従い行うことができる。機能を有するタンパク質の存在を示すレポーター遺伝子は、転写因子等のタンパク質因子が結合できる適切な発現制御配列部分（1つまたは複数）と、その転写因子等による活性化を測定できる構造遺伝子部分からなる。構造遺伝子部分は、その発現産物の活性または生産量（mRNAの生産量も含まれる）を当業者が測定可能なものであれば、いかなるペプチド、タンパク質をコードする遺伝子も用いることができる。たとえば、クロラムフェニコールアセチルトランスフェラーゼ、 β -ガラクトシダーゼ、ルシフェラーゼ等を用いることができ、その酵素活性を測定することで利用できる。

本発明において、オリゴキャッピング法とは、鈴木・菅野 実験医学別冊 遺伝子工学ハンドブック改訂第3版に記載のように、BAP, TAP, RNAリガーゼにより、キャップ構造を合成オリゴに置換する方法である。

本発明の方法は、インビトロ（*in vitro*）の系、あるいは細胞を用いて（*cell-based*）の系のどちらの方法でも良く、好ましくは細胞を用いた系である。細胞は、原核大腸菌をはじめとする原核生物、酵母、真菌等の微生物、及び昆虫や動物等の細胞のいずれでも良く、好ましくは動物細胞であり、293-EBNA細胞、NIH3T3細胞が例示できる。

機能を有するタンパク質の存在を示すレポーター遺伝子としては、本願明細書に示したNF- κ B依存レポーター遺伝子の他に、たとえばCREB（cAMP responsive element binding protein）結合配列あるいはAP-1（activator protein-1）結合配列をレポーター遺伝子の発現制御配列部分に有するレポーター遺伝子が挙げられる。たとえば、CREBを活性化する機能を有する遺伝子を取得したい場合は、CREB依存レポータープラスミドとオリゴキャッピング法で作製した完全長cDNAを含む発現ベクターを細胞に共導入し、その中からレポーター活性が上昇した発現ベクターを選ぶことによって、該目的を達成することができる。また、CREBを抑制する機能を有する遺伝子を取得したい場合は、

CREB依存レポータープラスミドとオリゴキャッピング法で作製した完全長 cDNA を含む発現ベクターを細胞に共導入し、その中からレポーター活性が減少した発現ベクターを選ぶことによって、該目的を達成することができる。この場合、細胞に何らかの刺激を加えた状態で行なっても良い。cDNA クローン（発現ベクター）の細胞への導入は、1 クローンでも良いし、複数のクローンを同時に導入しても良い。本発明の該方法の一例は、本願明細書実施例に詳細に記述してある。あるいは、完全長 cDNA を含む発現ベクターとレポーター遺伝子を細胞に導入した後、細胞を IL-1 あるいは TNF- α など刺激し、レポーター活性の上昇の弱いクローンを選ぶことによって、NF- κ B の活性化を抑制する機能を有する遺伝子を取得するためのスクリーニング系を構築することもできる。

しかしながら、本発明の該方法は、この方法に限定されるものではない。また、本発明の cDNA は、完全長 cDNA であるため、その 5' 末端の配列が mRNA の転写開始点であり、該 cDNA 配列をゲノムのヌクレオチド配列と比較することにより、該遺伝子のプロモーター領域を同定することに利用できる。ゲノムのヌクレオチド配列は、データベースに公知の配列として登録されている場合はその配列を利用できる。あるいは、該 cDNA を用いてたとえばハイブリダイゼーションによってゲノムライブラリーからクローニングし、ヌクレオチド配列を決めることもできる。このようにして、本発明の cDNA のヌクレオチド配列をゲノムの配列と比較することによって、その上流に存在する該遺伝子のプロモーター領域を同定することが可能である。さらに、このようにして同定した該遺伝子のプロモーター断片を用いて該遺伝子の発現を調べるレポータープラスミドを作製することができる。レポータープラスミドは、大方の場合、転写開始点からその上流 2 kb、好ましくは転写開始点からその上流 1 kb の DNA 断片をレポーター遺伝子の上流に組み込むことによって作製できる。さらに該レポータープラスミドは、該遺伝子の発現を増強あるいは減弱させる化合物のスクリーニングに利用できる。具体的には例えば、該レポータープラスミドで適当な細胞を形質転換し、一定時間培養した形質転換細胞に、被験物質を任意の量添加し、一定時間後の該細胞が発現するレポーター活性を測定し、被験物質を添加しない細胞のレポーター活性と比較することによりスクリーニングすることができる。これら

も本発明に含まれる。

また本発明は、配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177 または 179 で表されるヌクレオチド配列のうち少なくとも 1 以上を含むデータセットおよび／または配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178 および 180 で表されるアミノ酸配列のうち少なくとも 1 以上を含むデータセットを保存したコンピュータ読み込み可能媒体に関する。

さらに本発明は、上記に記載の媒体上のデータと他のヌクレオチド配列のデータを比較して相同性の算出を行う方法に関する。すなわち、本発明の遺伝子およびアミノ酸配列は、その 2 次元および 3 次元構造を決定し、たとえば同様の機能を有する相同性の高いさらなる配列を同定するための貴重な情報源となる。これらの配列をコンピュータ読み込み可能媒体に保存し、ついで既知の高分子構造プログラムにおいて保存したデータを用いて、GCG のような既知検索ツールを用いてデータベースを検索すれば、データベース中の、ある相同性を有する配列を

見出すことは容易である。

コンピュータ読み取り可能媒体は情報またはデータを保存するのに用いる物体のいずれの組成物であってもよく、たとえば、市販フロッピーディスク、テープ、チップ、ハードドライブ、コンパクトディスク、およびビデオディスク等がある。また、本媒体上のデータは、他のヌクレオチド配列のデータと比較して相同性の算出を行なう方法を可能にする。この方法には、本発明ポリヌクレオチド配列を含む第一のポリヌクレオチド配列をコンピュータ読み込み可能媒体中に提供し、次いで、該第一のポリヌクレオチド配列を少なくとも一つの第二のポリヌクレオチドまたはポリペプチド配列と比較して相同性を同定する工程を含む。

本発明はまた、配列番号 2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177 または 179 から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質に関する。DNAプローブである複数の各種ポリヌクレオチドがスライドガラス等の特別に加工された基質上に固定され、次いで標識された標的ポリヌクレオチドを、固定化されたポリヌクレオチドとハイブリダイズさせ、それぞれのプローブからのシグナルを検出する。得られるデータは、解析され、遺伝子発現が測定される。

本発明はさらにまた、配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、1

11、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質に関する。このタンパク質を固定した不溶性基質と、生物由来の細胞抽出液とを混合し、不溶性基質上に捕獲された、診断あるいは新薬開発のために有効であることが期待されるタンパク質などの細胞由来の成分を、単離あるいは同定することができる。

実施例

以下に、実施例を挙げて本発明を詳しく説明するが、本発明は、これらの例に何ら限定されるものではない。

(実施例1) オリゴキャッピング法を用いた完全長cDNAライブラリーの作製

(1) ヒト肺線維芽細胞 (Cryo NHLF) からのRNA調製

ヒト肺線維芽細胞 (Cryo NHLF : 三光純薬株式会社より購入) を、添付のプロトコールに従って培養した。10cmシャーレ50枚まで継代培養した後、セルスクレーパーで細胞を回収した。次いで、回収した細胞からRNA抽出用試薬ISOGEN (ニッポンジーンより購入) を用いて全RNAを取得した。取得の具体的方法は、試薬のプロトコールに従った。次いで、オリゴdTセルロースカラムを用いて、全RNAからポリA+RNAを取得した。ポリA+RNA取得の具体的方法は、上記Maniatisの実験書に従った。

(2) マウスATDC5細胞からのRNA調製

マウスEC (embryonal carcinoma) 由来クローン化細胞株ATDC5 (Atsumi, T. et al. : Cell Diff. Dev., 30:p109-116(1990)) を10cmシャーレ50枚まで継代培養した後、上記(1)と同様の方法でポリA+RNAを取得した。ATDC5細胞の培養は、Atsumi, T. et al. : Cell Diff. Dev., 30:p109-116(1990)に記載の方法に従って培養した。

(3) オリゴキャッピング法による完全長 cDNA ライブラリー作製

上記ヒト肺線維芽細胞と ATDC 5 細胞のポリ A+RNA から、オリゴキャッピング法により完全長 cDNA ライブラリーをそれぞれ作製した。オリゴキャッピング法による完全長 cDNA ライブラリー作製の具体的方法は、菅野らの方法 [たとえば、Maruyama, K. & Sugano, S. Gene, 138: 171-174 (1994)、Suzuki, Y. et al. Gene, 200: 149-156 (1997)、鈴木・菅野 実験医学別冊 遺伝子工学ハンドブック改訂第3版] に従って作製した。

(4) プラスミド DNA の調製

上記実施例で作製した完全長 cDNA ライブラリーを、エレクトロポレーション法によって大腸菌 TOP10 株に形質転換した後、100 μ g/ml アンピシリンを含有する LB 寒天培地に塗布し、37℃で一晩インキュベートした。続いて、アンピシリン含有 LB 寒天培地上で生育した大腸菌のコロニーから、QIAGEN 社の QIAwell 96 Ultra Plasmid Kit を用いてプラスミドを回収した。具体的方法は、QIAwell 96 Ultra Plasmid Kit に添付のプロトコールに従った。

(実施例 2) NF- κ B を活性化する作用を有する DNA のクローニング

(1) NF- κ B を活性化する作用を有するタンパク質をコードする cDNA のスクリーニング

293-EBNA 細胞 (Invitrogen 社より購入) を細胞培養用 96 穴プレートに 1×10^4 Cells/100 μ l/well となるように、5% FBS 存在下の DMEM 培地にまき、24 時間 37℃で培養した (5% CO₂ 存在下)。次いで、FuGENE 6 (Roche 社より購入) を用いて、pNF κ B-Luc (STRATAGENE 社より購入) 50 ng と、上記実施例 1. (4) で調製した完全長 cDNA 発現ベクター 2 μ l を 1 ウェルに共導入した。導入の方法は添付のプロトコールに従った。24 時間 37℃で培養後、ロングタームルシフェラーゼアッセイシステム、ピッカジーン LT 2.0 (東洋インキ社) を用いて添付されている説明書に従い、NF- κ B のレポーター活性 (ルシフェラーゼ活性) を測定した。なおルシフェラーゼ活性は、Perkin Elmer 社

のWallac ARVOTMST 1420 MULTILABEL COUNTERを用いて行った。

(2) ヌクレオチド配列の決定

上記スクリーニングを155000クローン行い、ルシフェラーゼ活性が対照実験（完全長cDNA発現ベクターの代わりに、空ベクターpME18S-FL3を導入した細胞のルシフェラーゼ活性）と比べて5倍以上上昇しているプラスミドを選抜し、まず、クローニングされているcDNAの5'側（シークエンスプライマー：5'-CTTCTGCTCTAAAAGCTGCG-3'（配列番号181）と3'側（シークエンスプライマー：5'-CGACCTGCAGCTCGAGCACA-3'（配列番号182）からそれぞれone-passシークエンスを行ない、できる限り長く決定した。なお、ヌクレオチド配列決定のための試薬や方法は、Thermo Sequenase II Dye Terminator Cycle Sequencing Kit（アマシャムファルマシア社）、あるいはBigDye Terminator Cycle Sequencing FS Ready Reaction Kit（アプライドバイオシステムズ社）を用い、ABI PRISM 377シークエンサー、あるいは、ABI PRISM 3100シークエンサーを用い、各々キットに添付されている説明書に従って行なった。

(3) 得られたクローンのデータベース解析

得られたヌクレオチド配列について、GenBankに対するBLAST (Basic local alignment search tool) [S. F. Altschul et al., J. Mol. Biol., 215: 403-410 (1990)] 検索を行なった。その結果、148クローンがNF- κ Bを活性化する作用を有する新規のタンパク質をコードする90種類の遺伝子であった。

(4) 全長シークエンス

90種類の新規のクローンについて全長ヌクレオチド配列（配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、

80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179)を決定し、タンパク質をコードする部分(オープンリーディングフレーム)のアミノ酸配列(配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178および180)を予想した。

(実施例3) NF- κ Bの活性化を阻害する化合物のスクリーニング

293-EBNA細胞を細胞培養用96wellプレートに、 1×10^4 Cells/100 μ l/wellの細胞数になるように、5%FBS存在下のDMEM培地にまき、5%CO₂存在下、37℃で24時間培養した。次いで、FuGENE6を用いて、上記実施例2で得た、配列番号5、9、17、21、35、37、41、53、57、63、67、71、75、81、87、91、93、97、121、123、129、154、158、162、168、170、172、176または178のNF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子を含む発現ベクター50ngと、レポータープラスミドpNF κ B-Luc50ngを1wellに共導入した。1時間後、プロテアソーム阻害剤であることが知られているMG-132(CALBIOCHEMより購入)(Uehara T. et. al. J. Biol. Chem. 274 p15875-15882(1999)、Wang XC. et al. Invest.

O p h t h a l m o l . V i s . S c i . 4 0 p 4 7 7 - 4 8 6) を終濃度 0. 1 μ M、0. 5 μ M、1. 0 μ M、1 0 μ Mになるようにそれぞれ培養液中加入した。3 7℃で2 4時間培養後、ピッカジーンLT 2. 0を用いてレポーター活性を測定した。その結果、MG 1 3 2はレポーター遺伝子の発現を抑制した（図 1 から図 2 9）。

産業上の利用性

本発明により、産業上有用性の高いNF- κ Bを活性化作用を有するタンパク質やそれらの遺伝子が提供された。本発明のタンパク質やそれらの遺伝子により、NF- κ Bの過剰な活性化、又は阻害が関与する疾患の治療や予防に有用な化合物のスクリーニング、さらにそのような疾患の診断薬を作製することが可能である。更に本発明の遺伝子は、遺伝子治療に用いられる遺伝子ソースとしても有用である。

本明細書で引用した全ての刊行物、特許及び特許出願をそのまま参考として本明細書にとり入れるものとする。

請 求 の 範 囲

1. 以下の (a) または (b) の精製されたタンパク質。

(a) 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178 または 180 のいずれかで表されるアミノ酸配列からなるタンパク質。

(b) 配列番号 1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178 または 180 のいずれかにおいて 1 若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつ NF- κ B (Nuclear factor kappa B) を活性化する作用を有するタンパク質。

2. 請求項 1 記載のタンパク質とその全長にわたり 95% 以上のアミノ酸配列の同一性を有するタンパク質であり、かつ NF- κ B を活性化する作用を有する精製されたタンパク質。

3. 以下の(a)または(b)のタンパク質をコードするヌクレオチド配列を包含する単離されたポリヌクレオチド。

(a) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかで表されるアミノ酸配列からなるタンパク質。

(b) 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180のいずれかにおいて1若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつNF- κ Bを活性化する作用を有するタンパク質。

4. 以下の(a)～(c)のいずれかのポリヌクレオチド配列を含む単離されたポリヌクレオチド。

(a) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、

48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかで表されるポリヌクレオチド配列。

(b) (a) のポリヌクレオチド配列と相補的なポリヌクレオチド配列を有するポリヌクレオチドとストリンジェントな条件下でハイブリダイズし、かつNF- κ Bを活性化作用を有するタンパク質をコードするポリヌクレオチド配列。

(c) 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179のいずれかにおいて、1若しくは複数個のヌクレオチドが欠失、置換若しくは付加されたポリヌクレオチド配列からなり、かつNF- κ Bを活性化作用を有するタンパク質をコードするポリヌクレオチド配列。

5. 請求項3記載のポリヌクレオチドと全長にわたり少なくとも95%以上の同一性を有し、かつNF- κ Bを活性化作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

6. 請求項4記載のポリヌクレオチドと全長にわたり少なくとも95%以上の

同一性を有し、かつNF- κ Bを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

7. 請求項3～6のいずれか1項に記載のポリヌクレオチドによりコードされる精製されたタンパク質。

8. 請求項3～6のいずれか1項に記載のポリヌクレオチドを含有する組換えベクター。

9. 請求項8に記載の組換えベクターを含む形質転換された細胞。

10. 請求項1または2に記載のタンパク質が膜タンパク質である場合における、請求項9記載の細胞の膜。

11. (a) 請求項3～6のいずれか1項に記載の単離されたポリヌクレオチドがコードするタンパク質を発現する条件下で該ポリヌクレオチドを含有する形質転換された細胞を培養し、

(b) 培養物からタンパク質を回収する、
ことを含むタンパク質の製造方法。

12. (a) 個体のゲノムにおける請求項1、2または7に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および／または

(b) 該個体に由来するサンプル中での該タンパク質の発現量を分析する、
ことを含む、該個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法。

13. 以下の工程を含むNF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングする方法。

(a) NF- κ Bを活性化するタンパク質をコードする遺伝子、およびNF- κ Bの活性化に対応した、検出可能なシグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された細胞を培養する工程、

(c) 該形質転換された細胞と1あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、および

(e) 該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物を単離もしくは同定する工程。

14. 以下の工程を含む、医薬組成物を製造する方法。

(a) NF- κ Bを活性化する作用を有するタンパク質をコードする遺伝子、および検出可能なシグナルを提供しうる成分を細胞に提供する工程、

(b) 該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された宿主細胞を培養する工程、

(c) 該形質転換された宿主細胞と1あるいは複数個の候補化合物とを接触させる工程、

(d) 検出可能なシグナルを測定する工程、

(e) 該検出可能なシグナルの測定により活性化剤化合物および／または阻害剤化合物を単離もしくは同定する工程、および

(f) 単離または同定された化合物を医薬組成物として最適化する工程。

15. NF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットであって、

(a) NF- κ Bを活性化するタンパク質をコードする遺伝子、およびNF- κ Bの活性化後、検出可能なシグナルを提供しうる成分により形質転換された細胞、および

(b) 検出可能なシグナルを測定するための試薬

を含むキット。

16. 請求項1、2または7に記載のタンパク質に特異的に結合するモノクローナルあるいはポリクローナル抗体。

17. 請求項1、2または7に記載のタンパク質を抗原あるいはエピトープ含有フラグメントとして非ヒト動物に投与することからなる、請求項1、2または7に記載のタンパク質に特異的に結合するモノクローナルまたはポリクローナル抗体の製造方法。

18. NF- κ Bの活性化タンパク質の発現を阻害する、請求項3～6のいずれか1項に記載のポリヌクレオチドに相補的なアンチセンスオリゴヌクレオチド。

19. 請求項1、2または7に記載のタンパク質をコードするRNAの開裂により、NF- κ Bの活性化を阻害するリボザイム。

20. 炎症、自己免疫疾患、感染症、癌および骨疾患からなる群から選択される疾患の治療に有効な量の請求項13記載の方法でスクリーニングされた化合物および／または請求項16記載のモノクローナルまたはポリクローナル抗体および／または請求項18記載のアンチセンスオリゴヌクレオチドおよび／または請求項19記載のリボザイムを個体に投与することを含む疾患の治療法。

21. NF- κ Bの活性化を阻害または活性化するものとして請求項14に記載の方法により製造された医薬組成物。

22. 炎症、自己免疫疾患、癌、感染症、骨疾患、AIDS、神経変性疾患、または虚血性障害の治療のための請求項21記載の医薬組成物。

23. NF- κ Bに関連する疾患を患っている患者に請求項14記載の方法に

より製造された医薬組成物を投与することからなる炎症、自己免疫疾患、癌、感染症、骨疾患、AIDS、神経変性疾患、または虚血性障害を治療する方法。

24. 請求項16記載のモノクローナルまたはポリクローナル抗体を有効成分として含有する医薬組成物。

25. 請求項18記載のアンチセンスオリゴヌクレオチドを有効成分として含有する医薬組成物。

26. 対象疾患が炎症、自己免疫疾患、感染症、癌疾患、骨疾患、AIDS、神経変性疾患および虚血性障害からなる群から選択される、請求項24または25に記載の医薬組成物。

27. 機能を有する新規遺伝子の取得方法であり、少なくとも以下の工程を含む方法。

- (a) オリゴキャッピング法を用いて完全長cDNAライブラリーを作製し、
 - (b) 完全長cDNAおよび該機能を有するタンパク質の存在を示すシグナルを発する因子を含有するプラスミドを細胞中にコトランスフェクションし、さらに
 - (c) シグナルを発するプラスミドを選択する、
- 方法。

28. 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、16

7、169、171、173、175、177または179で表されるヌクレオチド配列のうち少なくとも1以上を含むデータセットおよび／または配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178および180で表されるアミノ酸配列のうち少なくとも1以上を含むデータセットを保存したコンピュータ読み込み可能媒体。

29. 請求項28に記載の媒体上のデータと他のヌクレオチド配列および／または他のアミノ酸配列のデータを比較して他のポリヌクレオチド配列および／またはアミノ酸配列との同一性の算出を行う方法。

30. 配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、132、134、136、138、140、142、144、146、148、150、151、153、155、157、159、161、163、165、167、169、171、173、175、177または179から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質。

31. 配列番号1、3、5、7、9、11、13、15、17、19、21、23、25、27、29、31、33、35、37、39、41、43、45、47、49、51、53、55、57、59、61、63、65、67、69、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、131、133、135、137、139、141、143、145、147、149、152、154、156、158、160、162、164、166、168、170、172、174、176、178または180で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質。

図1

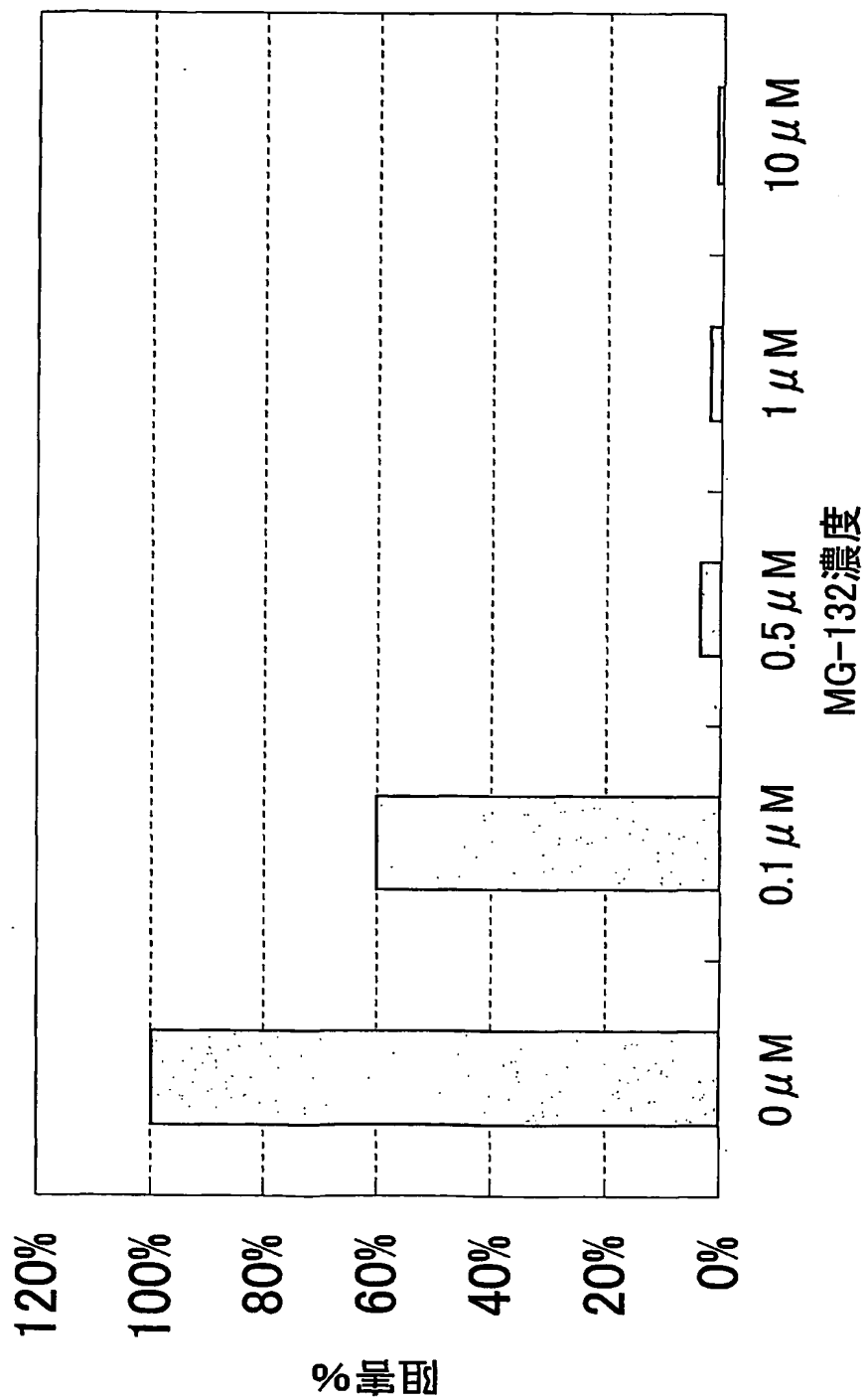


図2

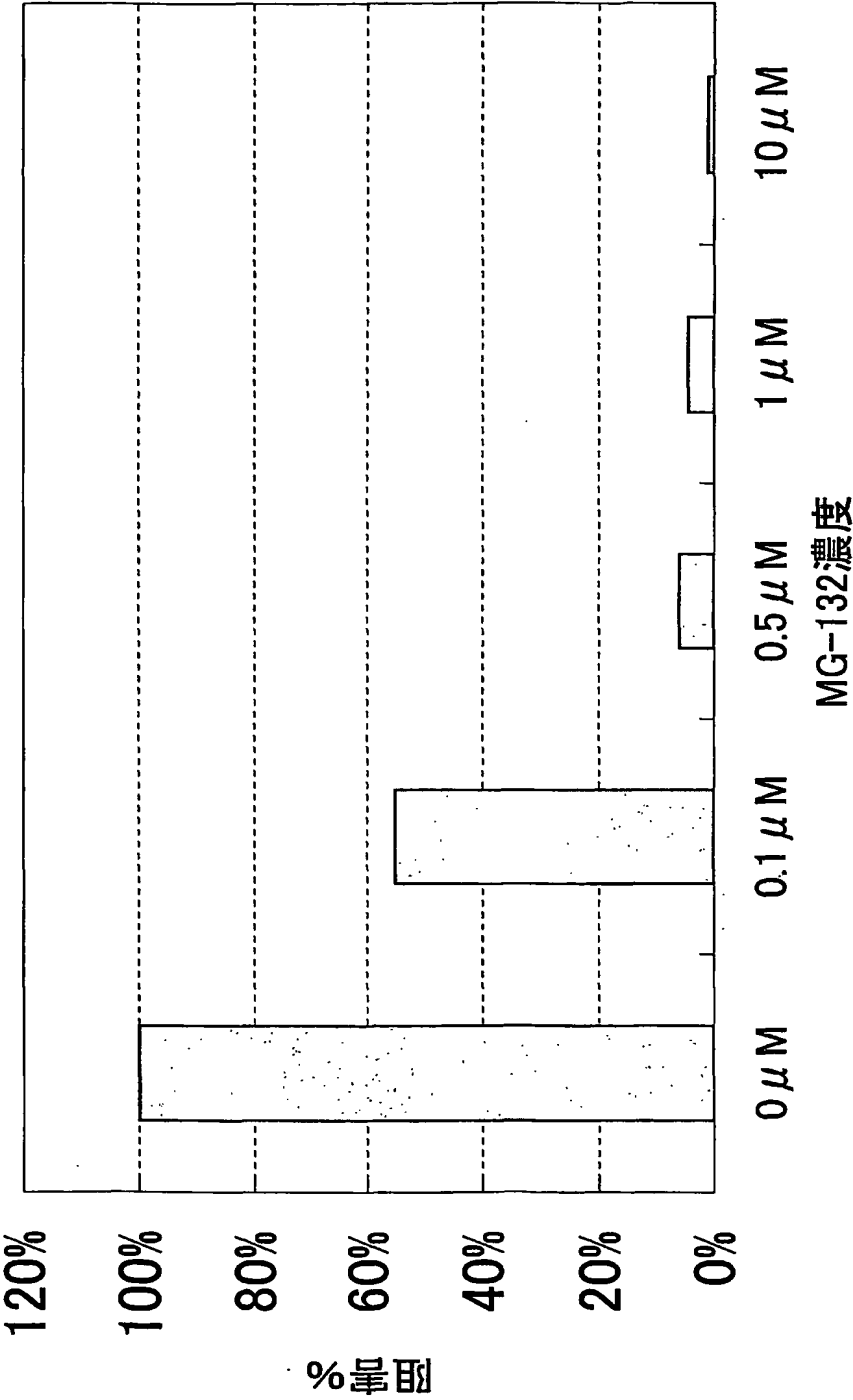


図3

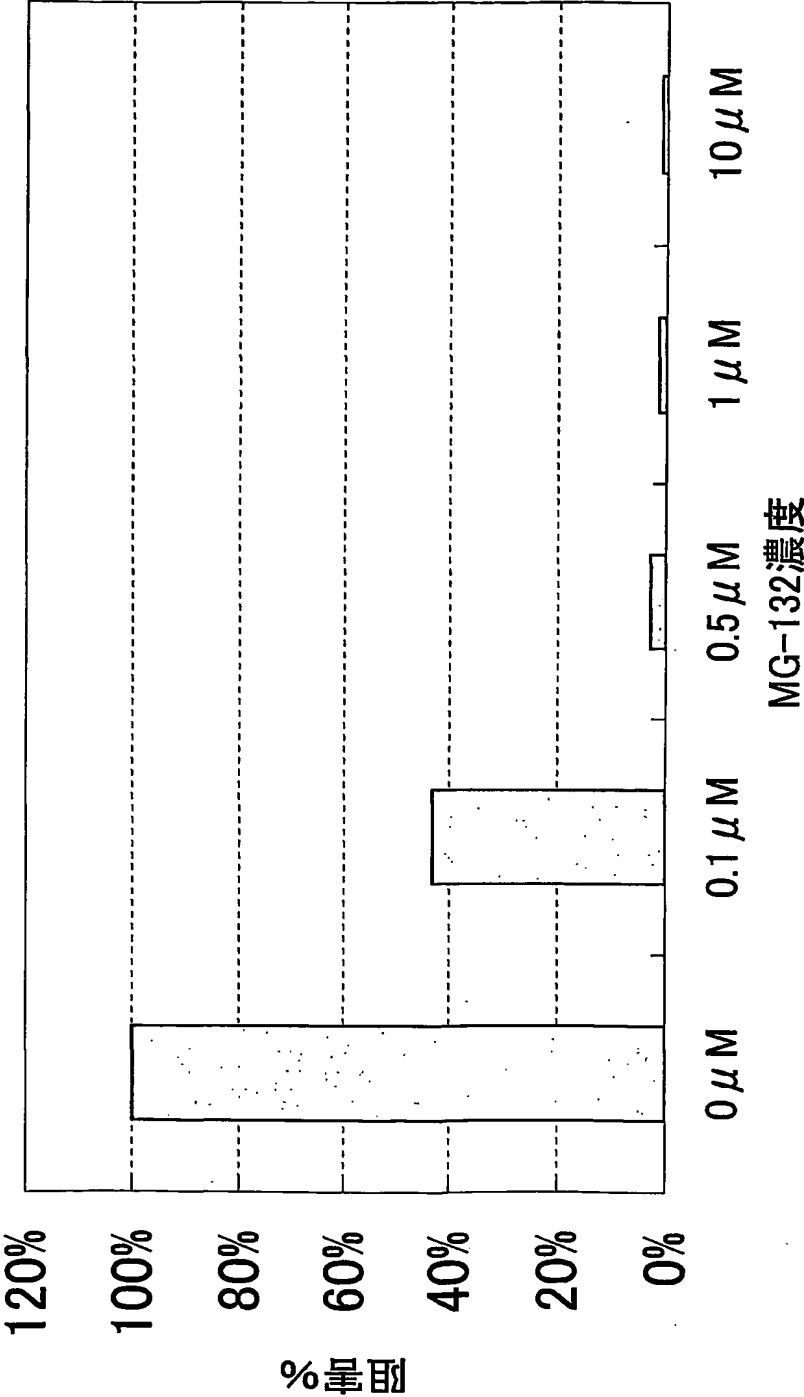


図4

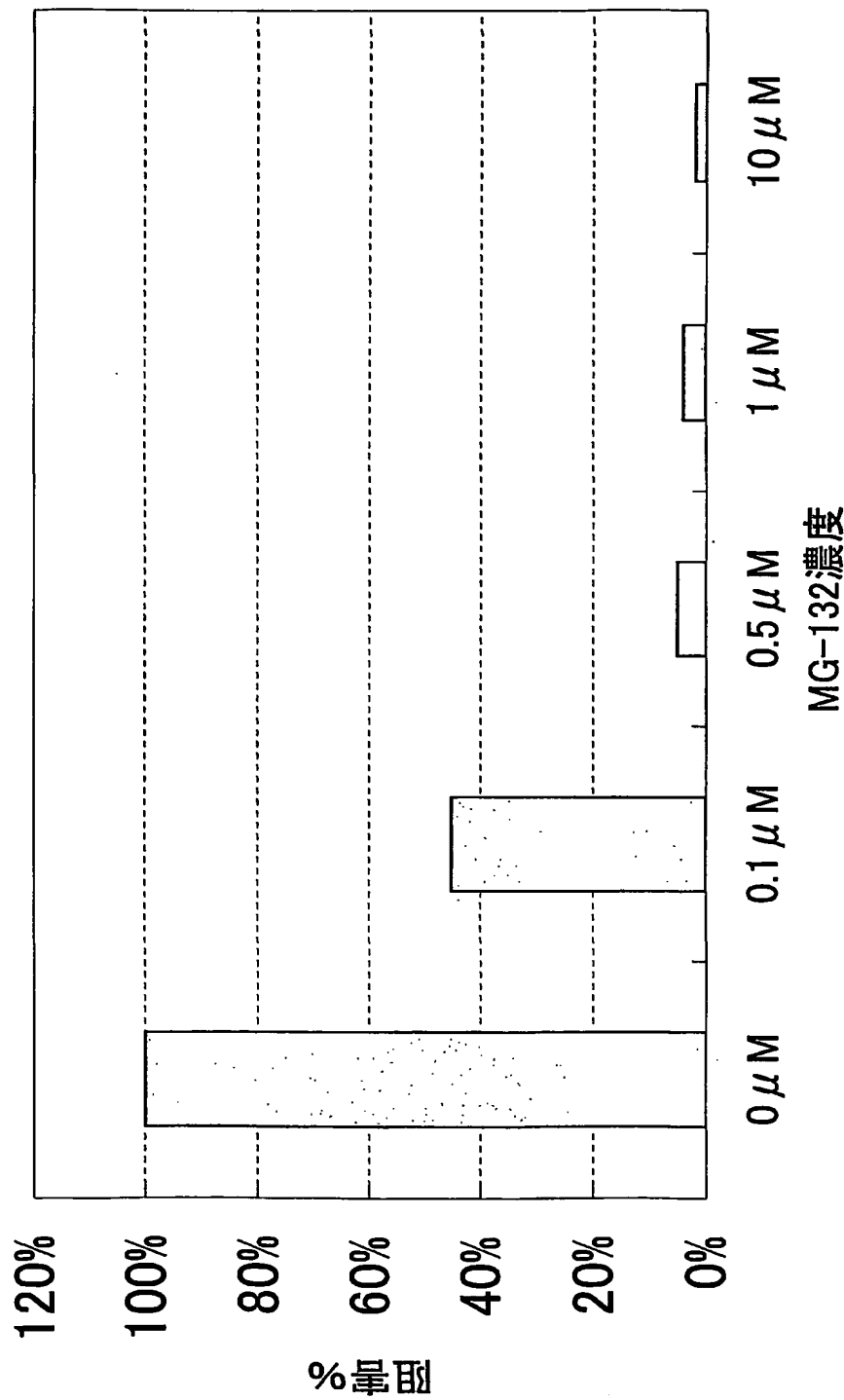


図5

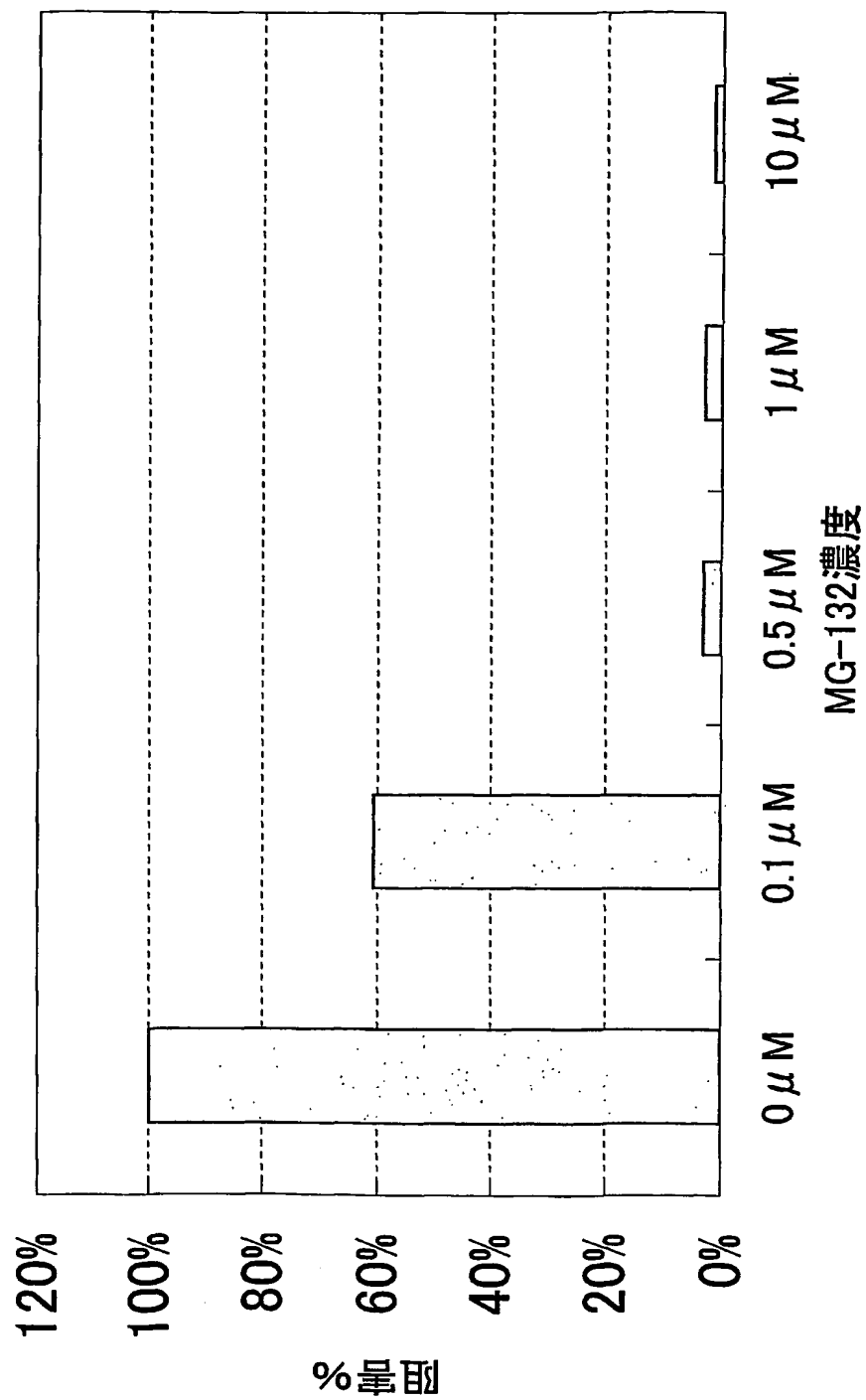


図6

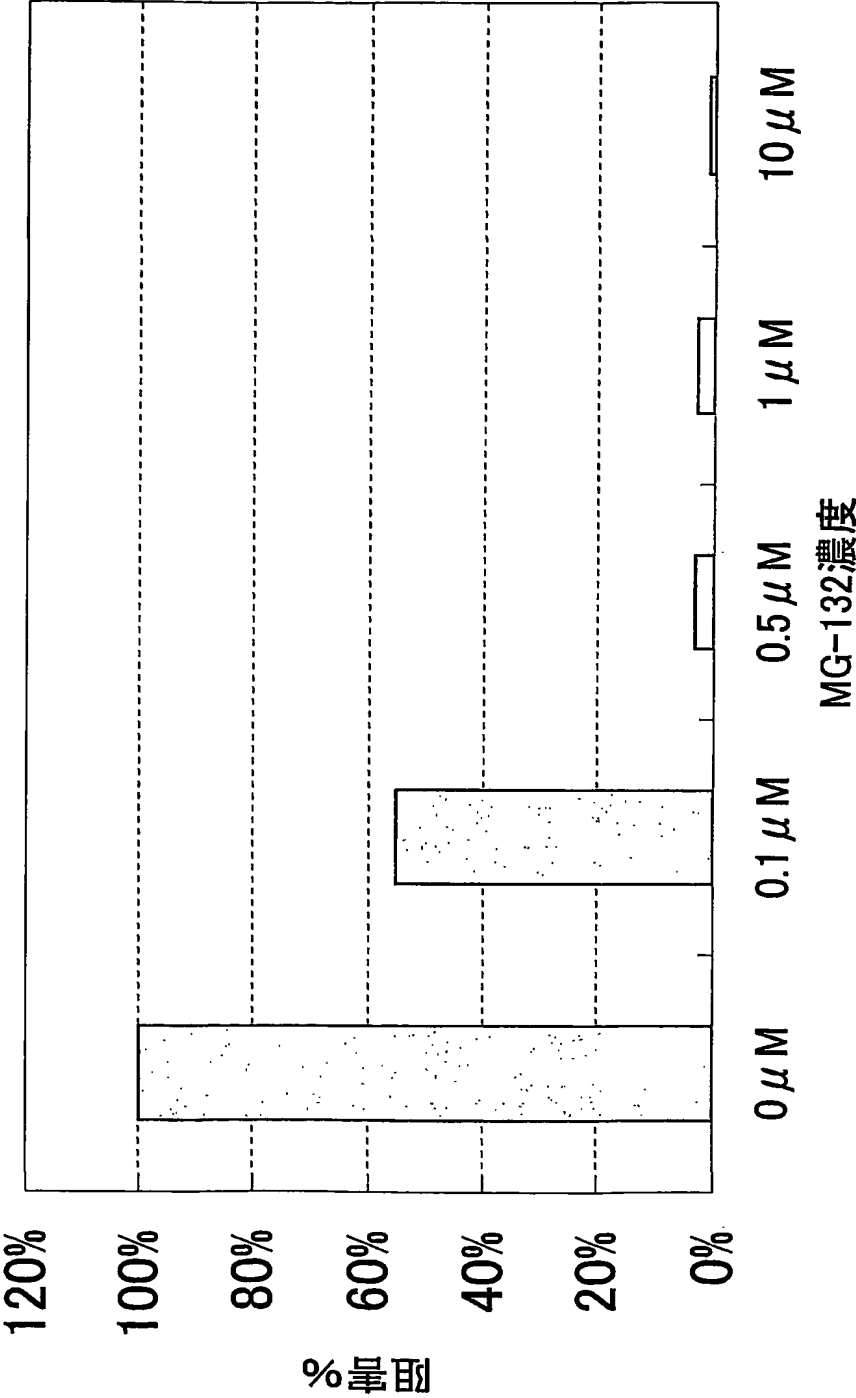


図7

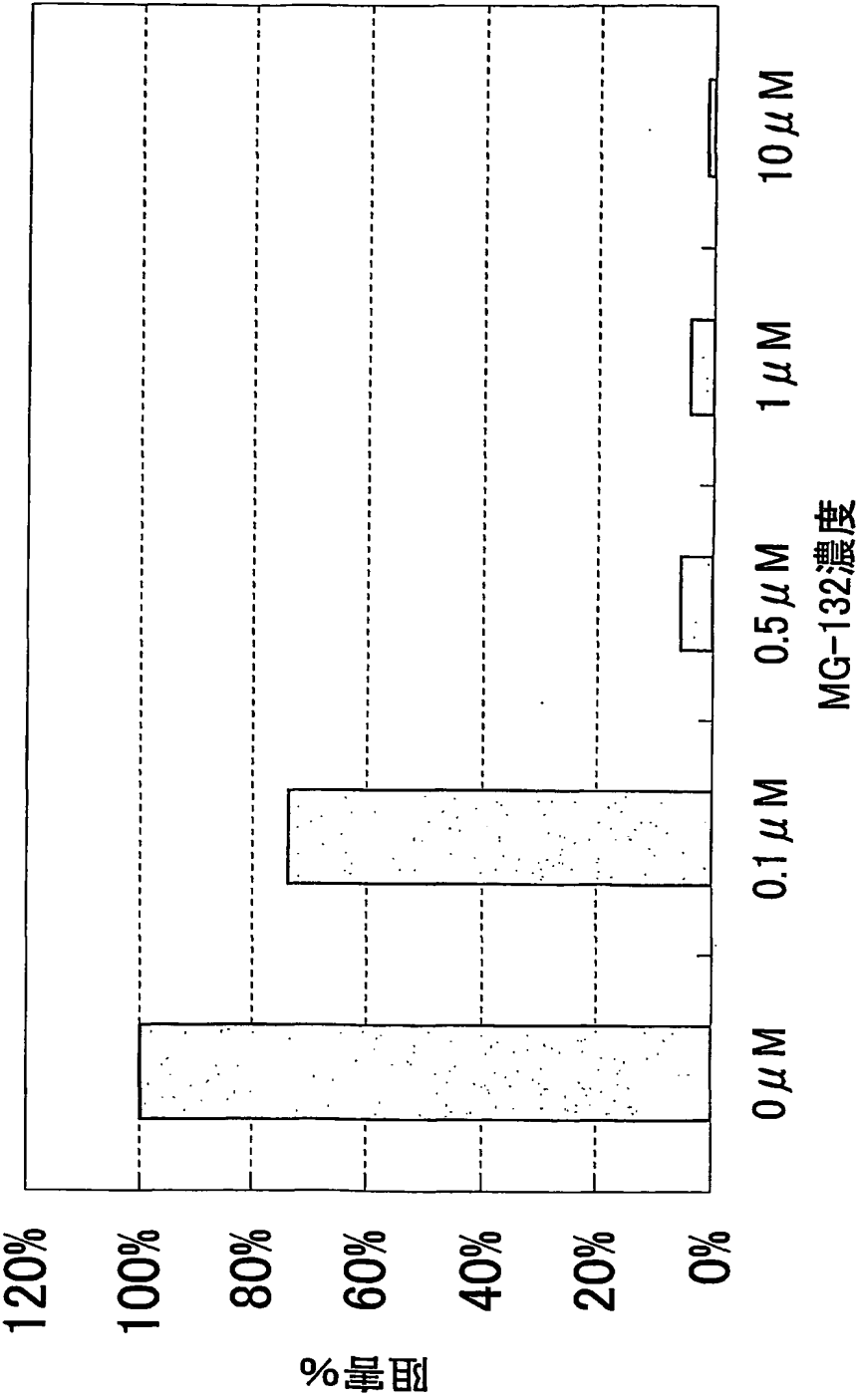


図8

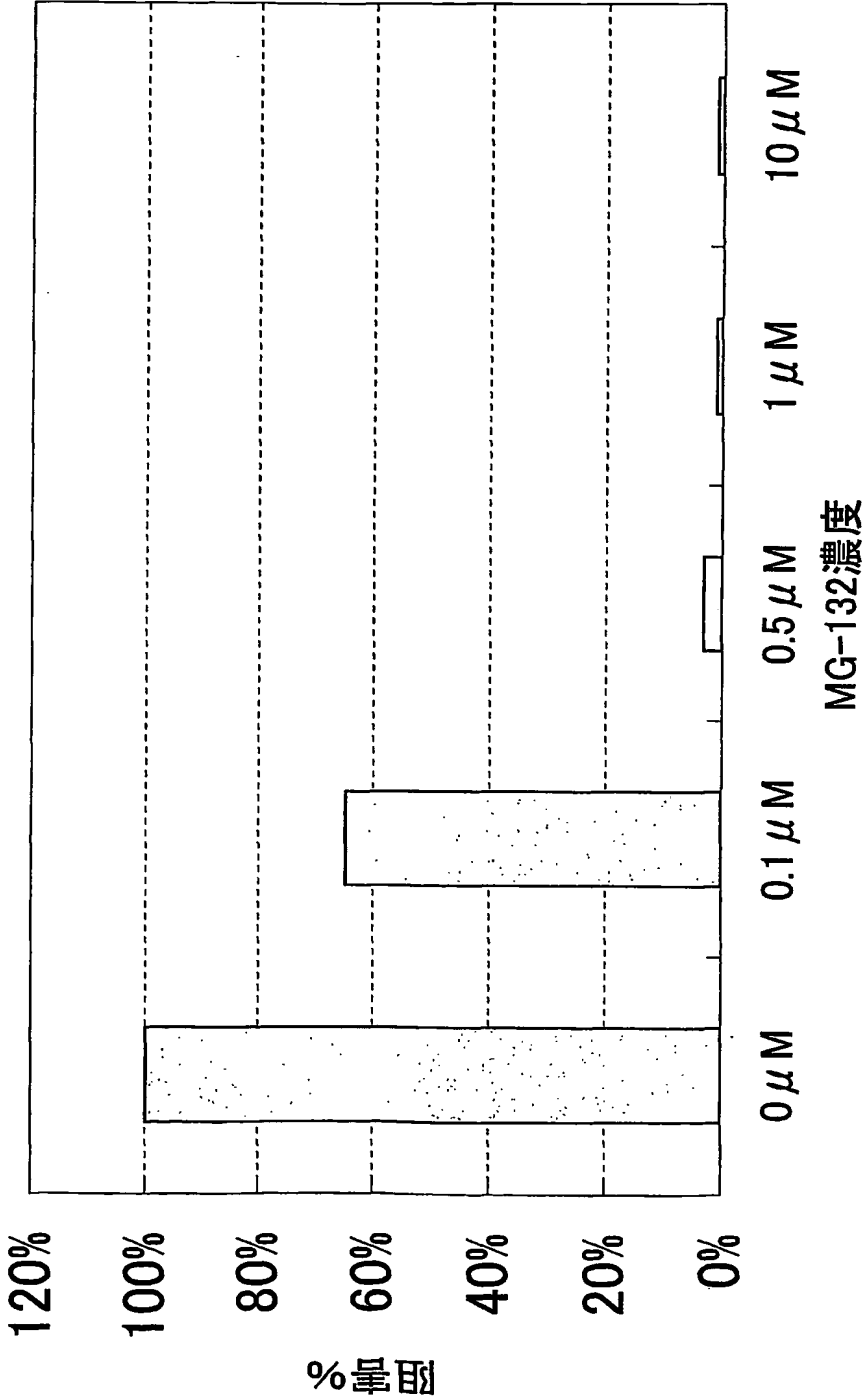


図9

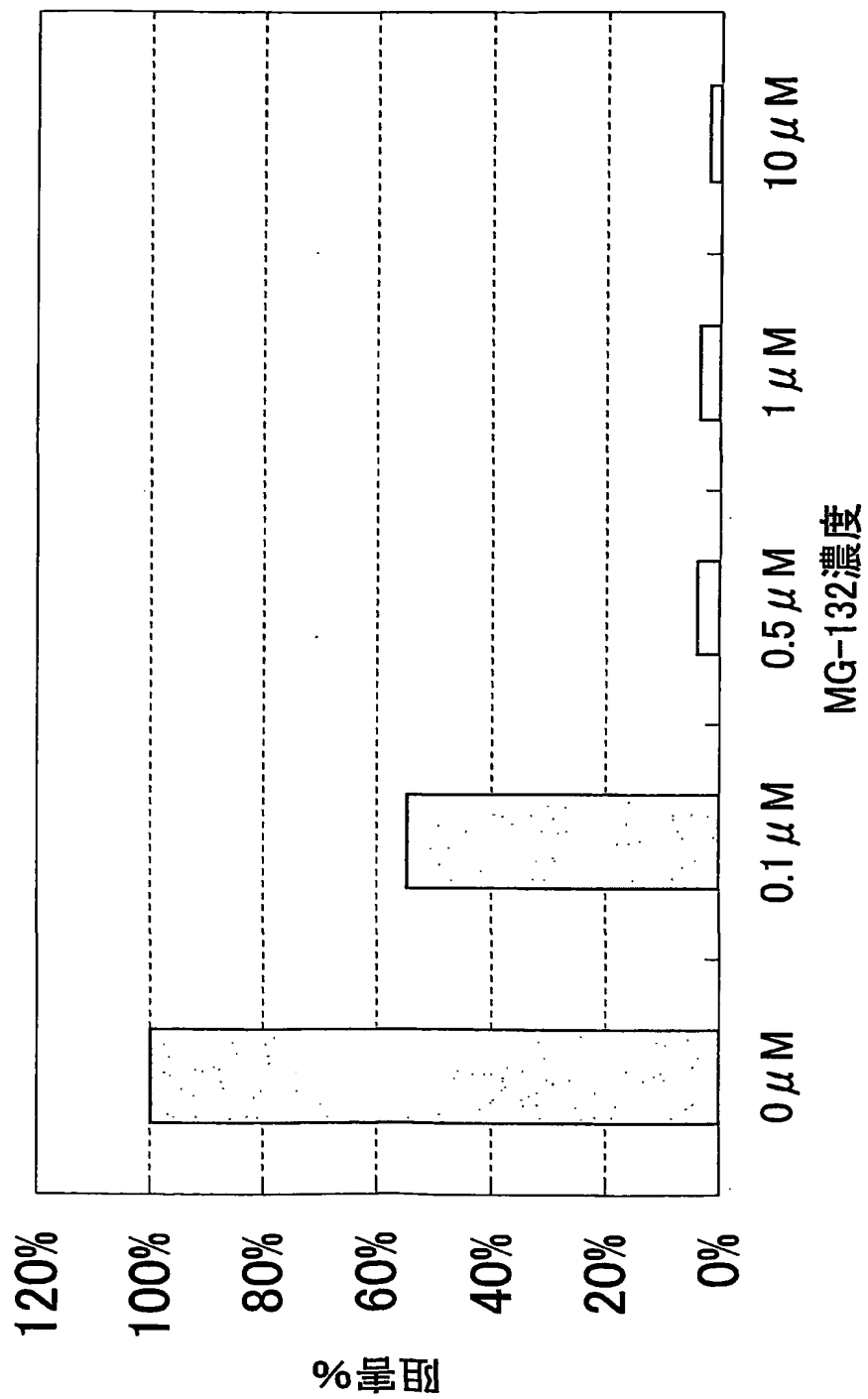


図10

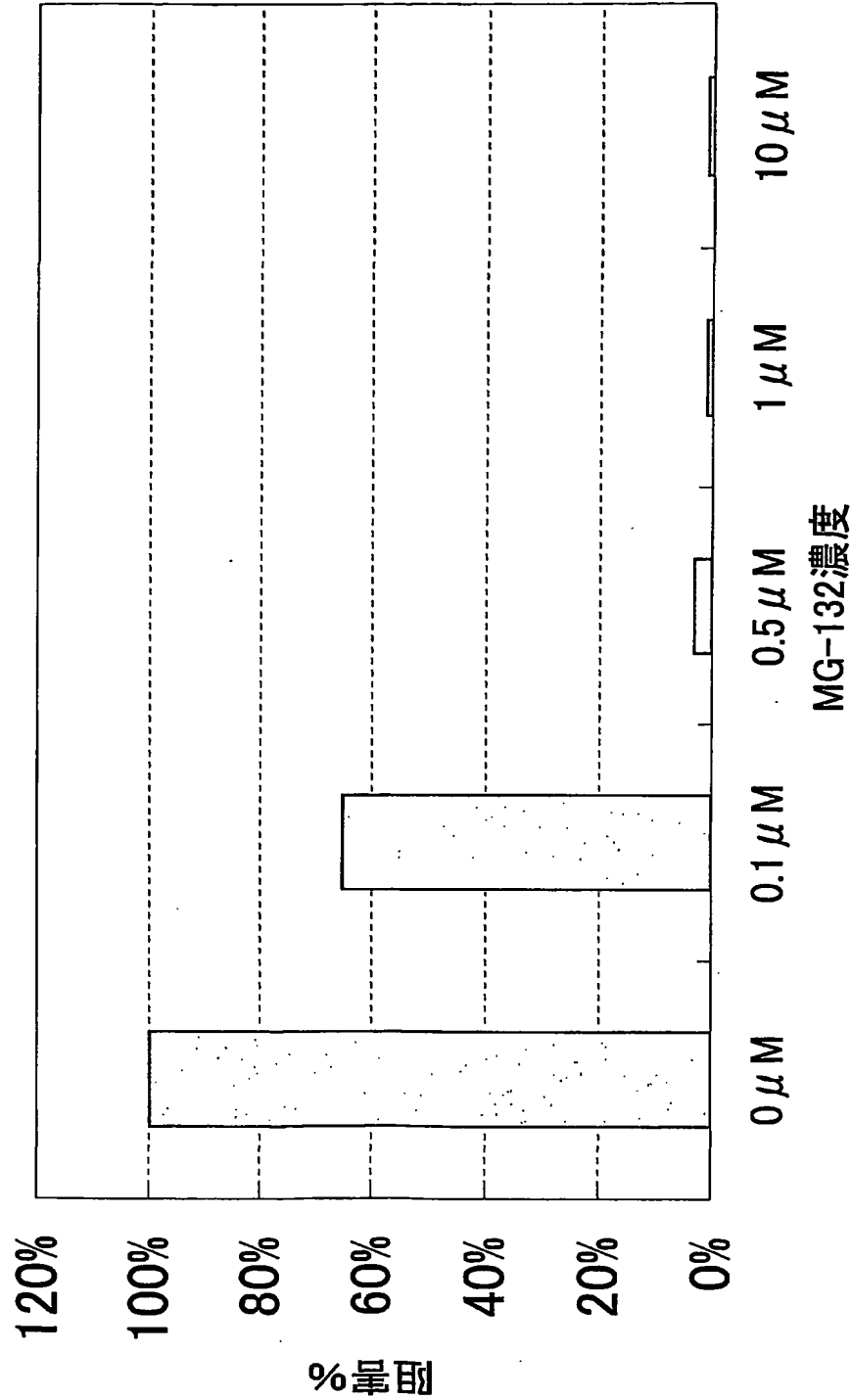


図11

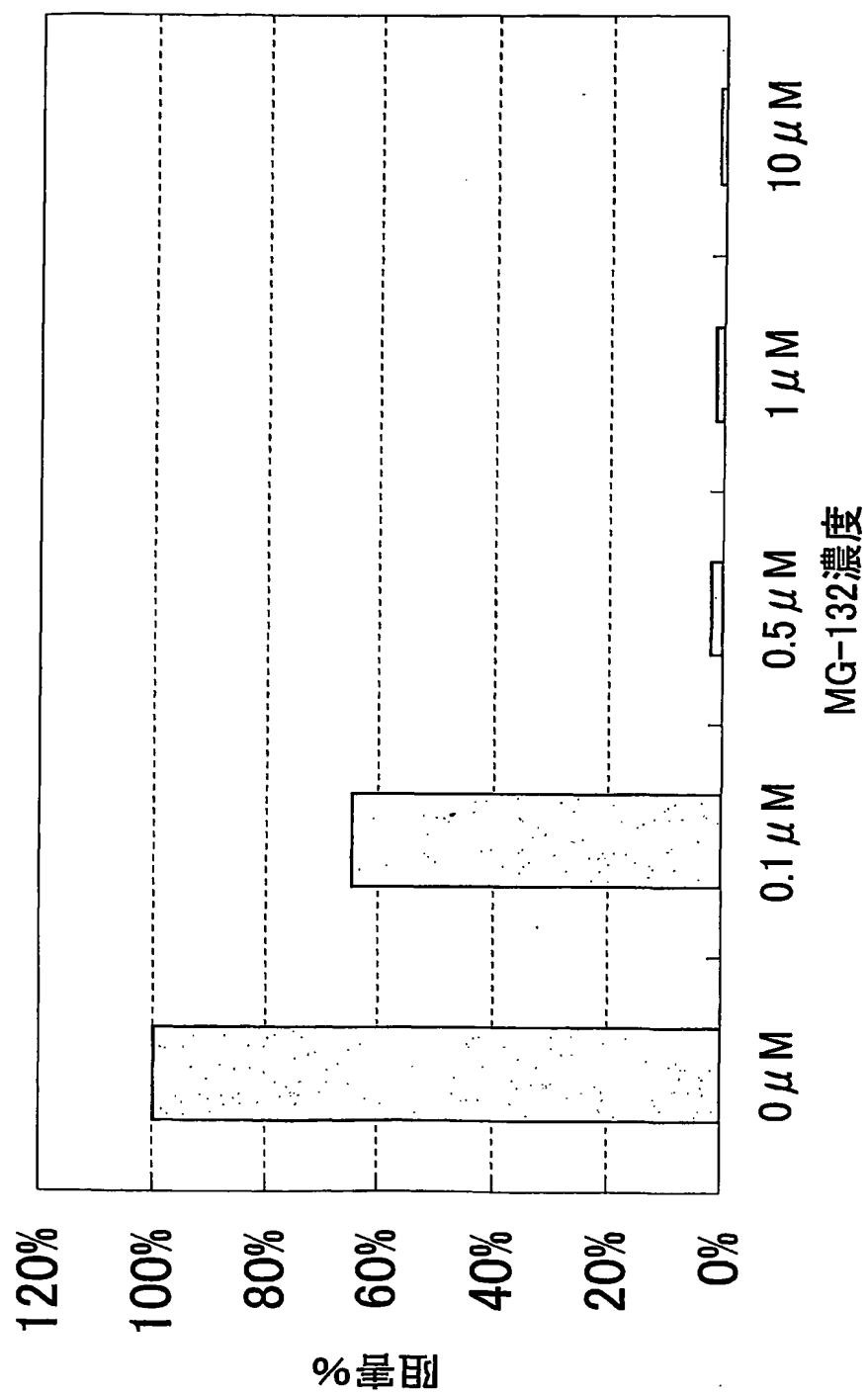


図12

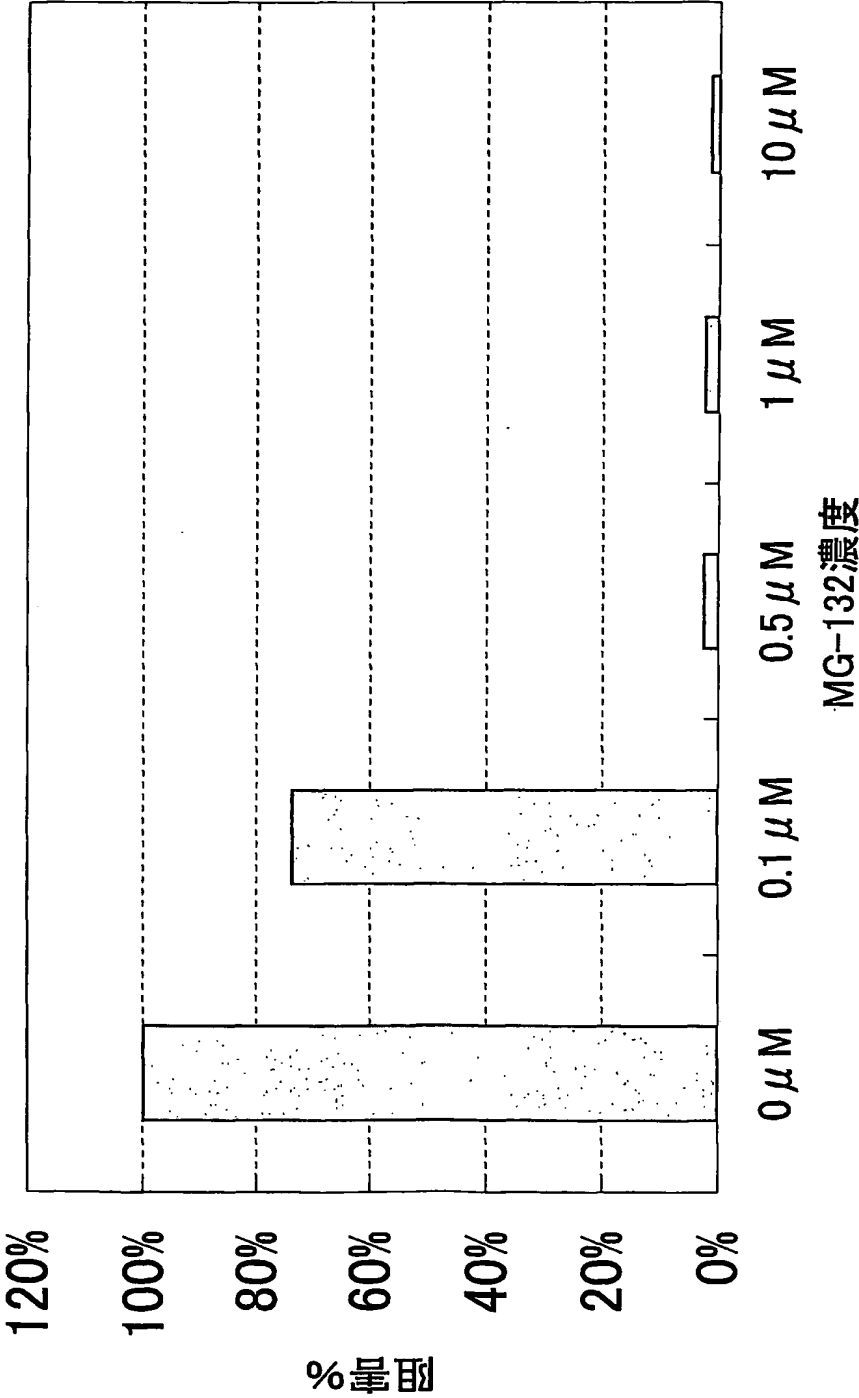


図13

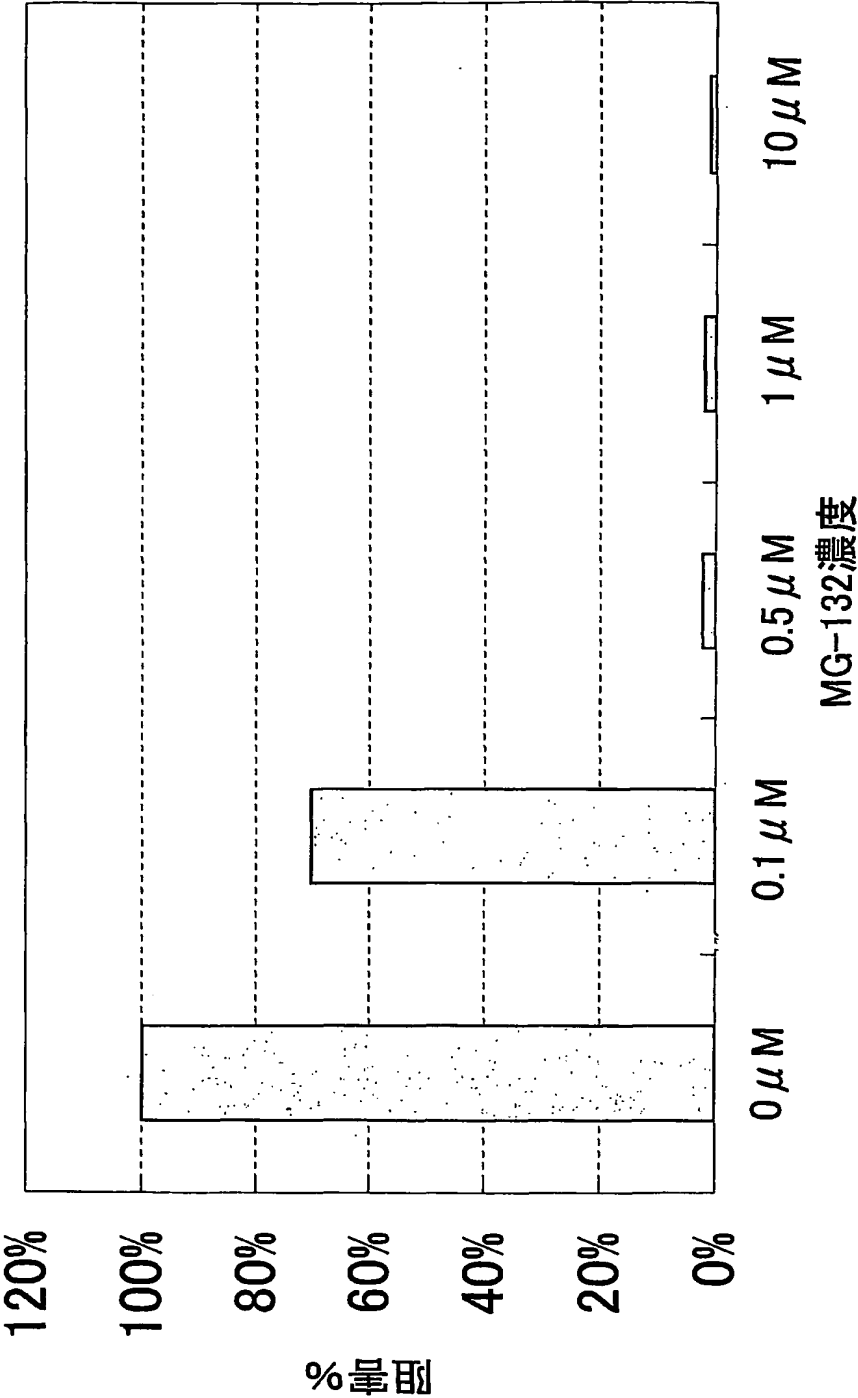


図14

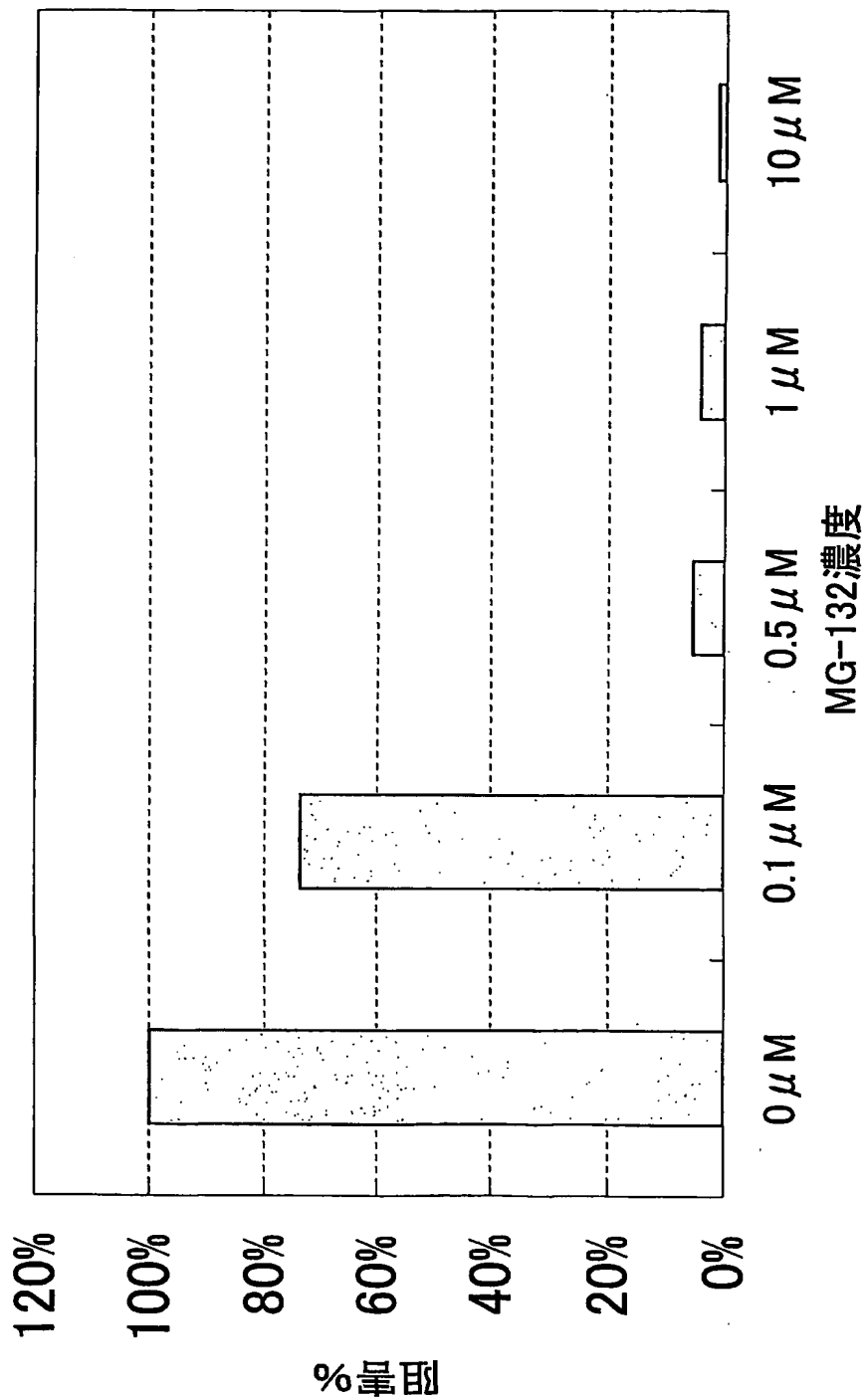


図15

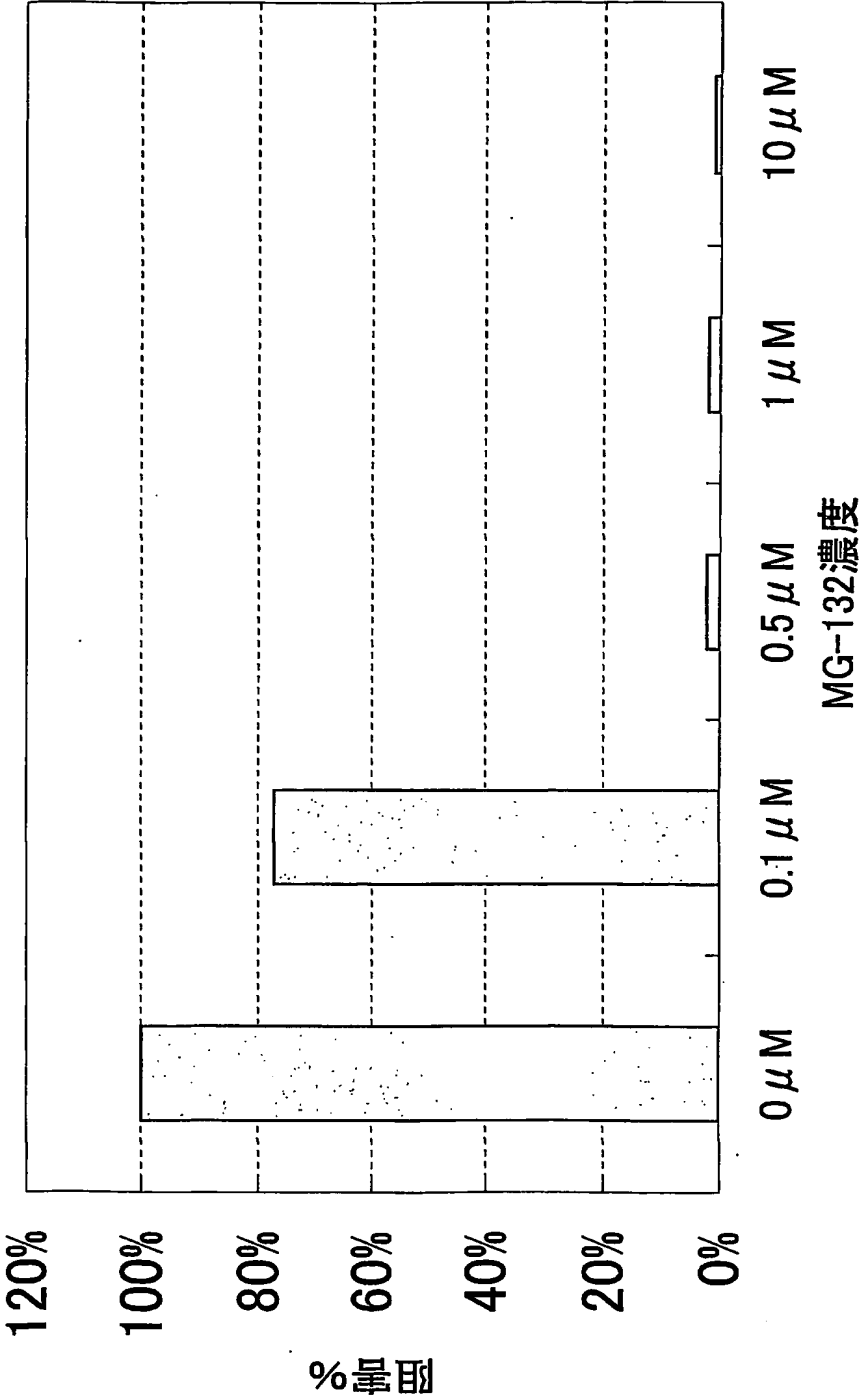


図16

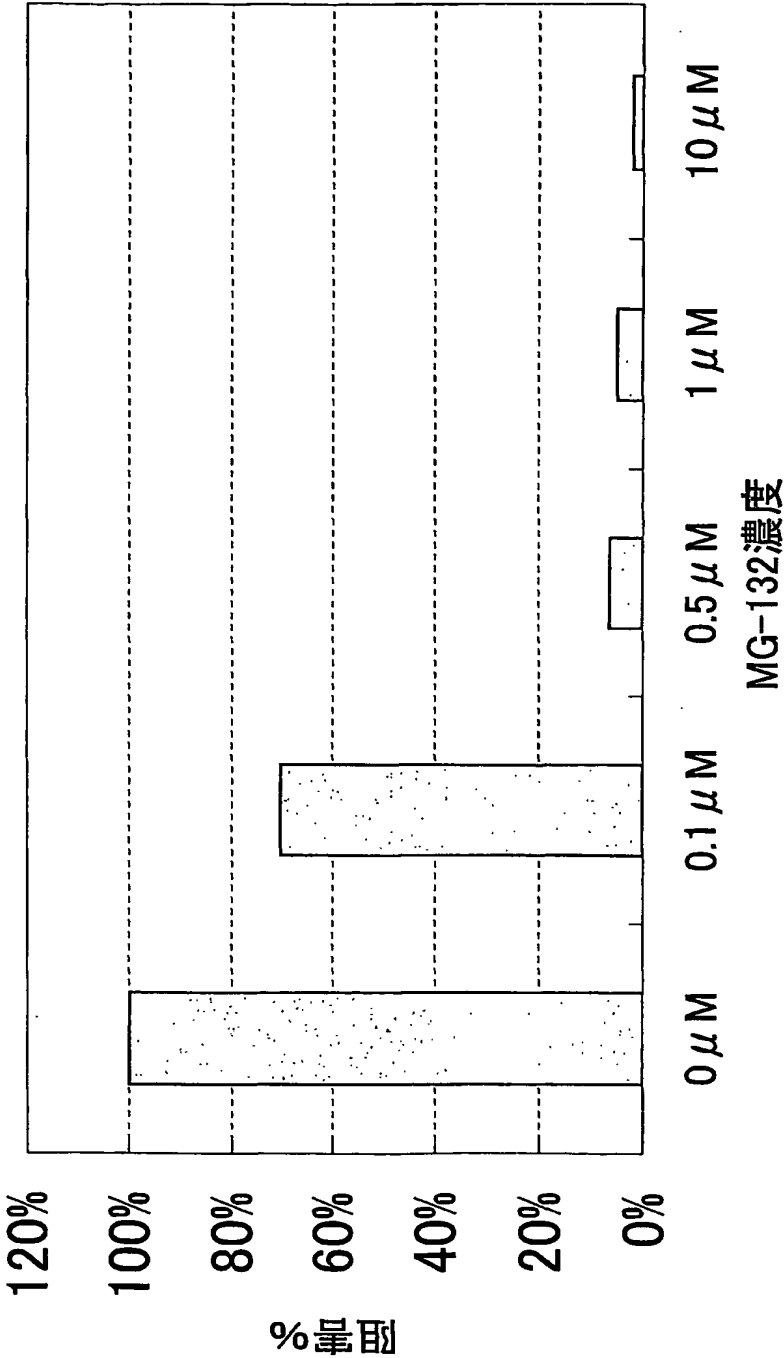


図17

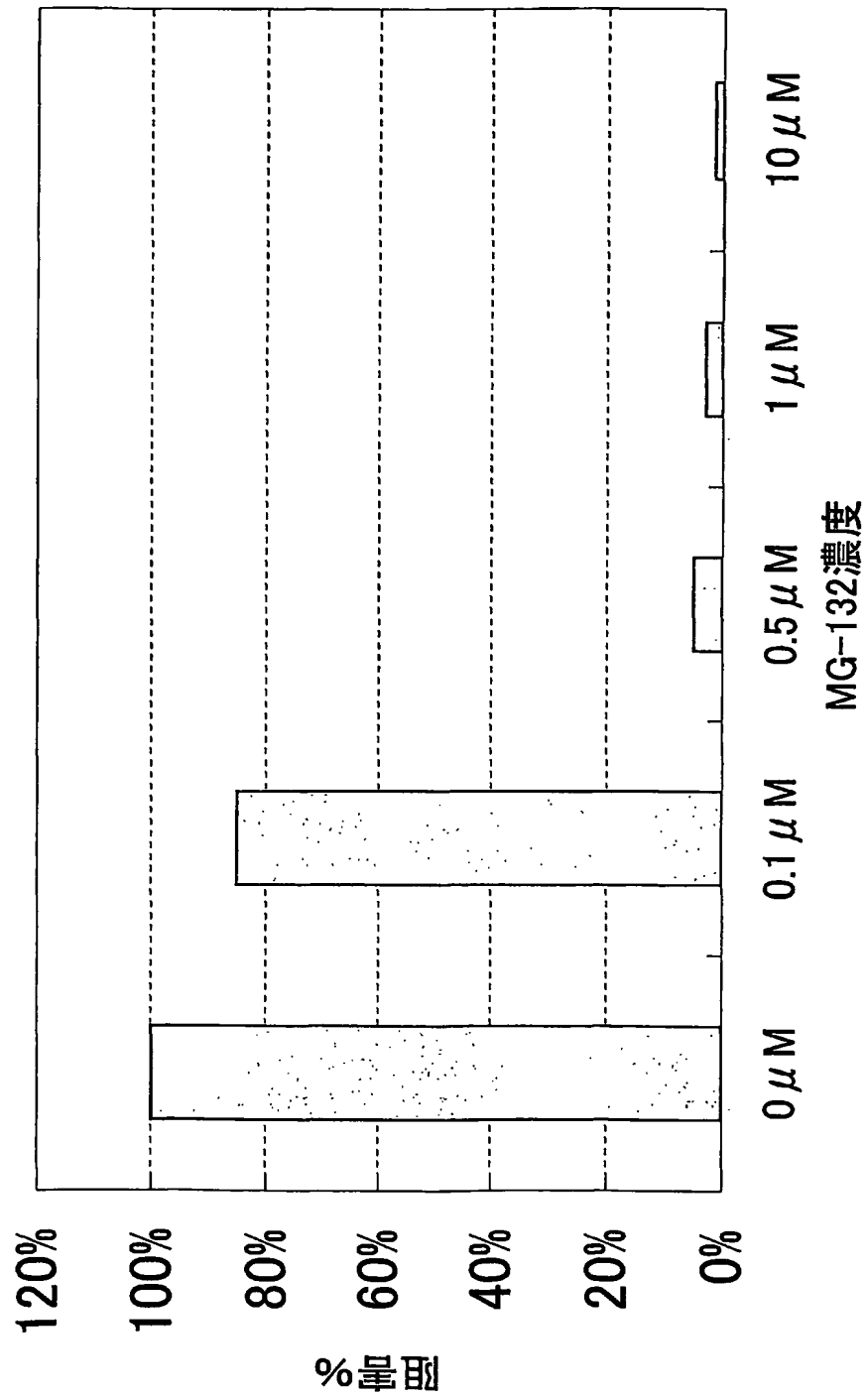


図18

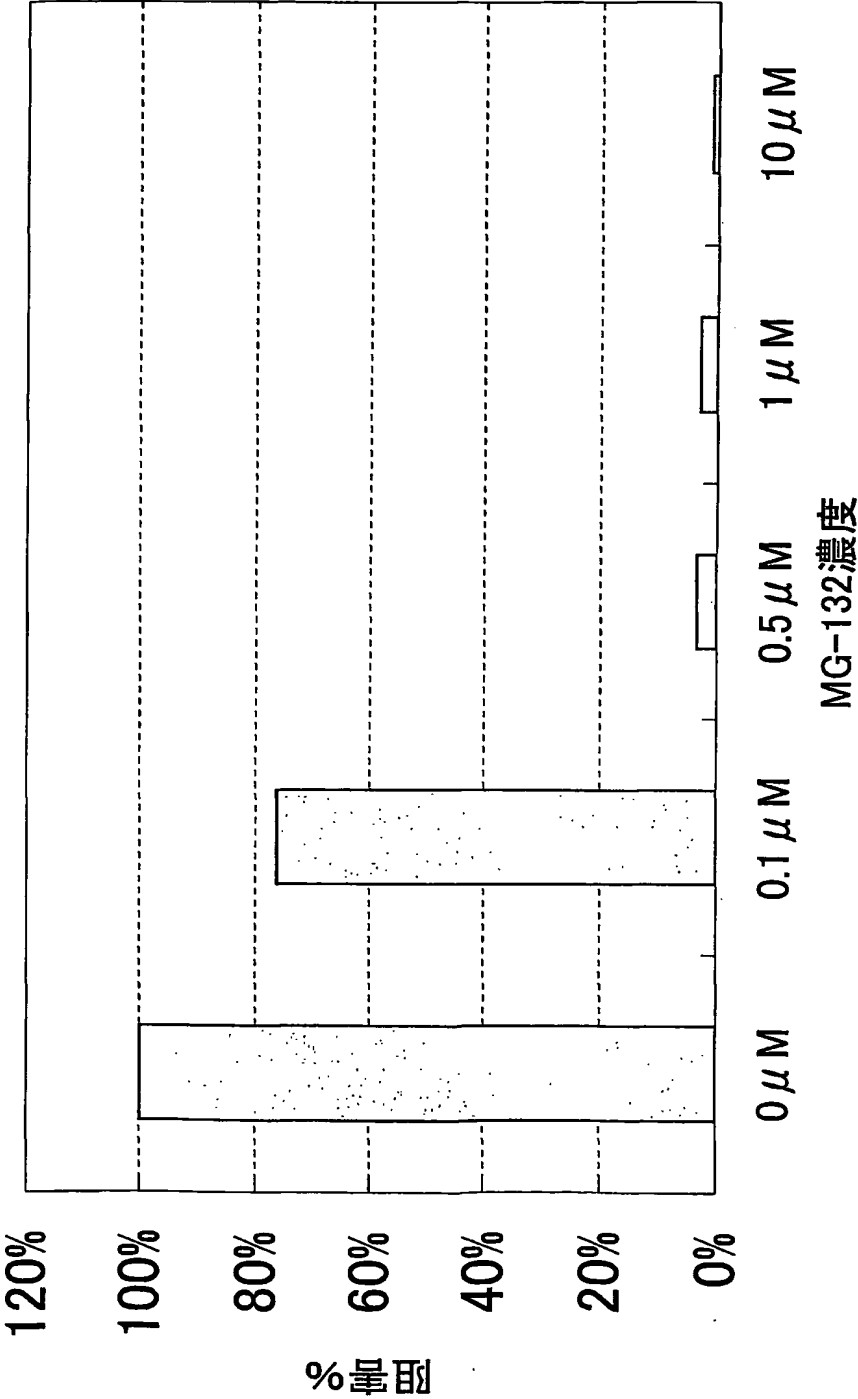


図19

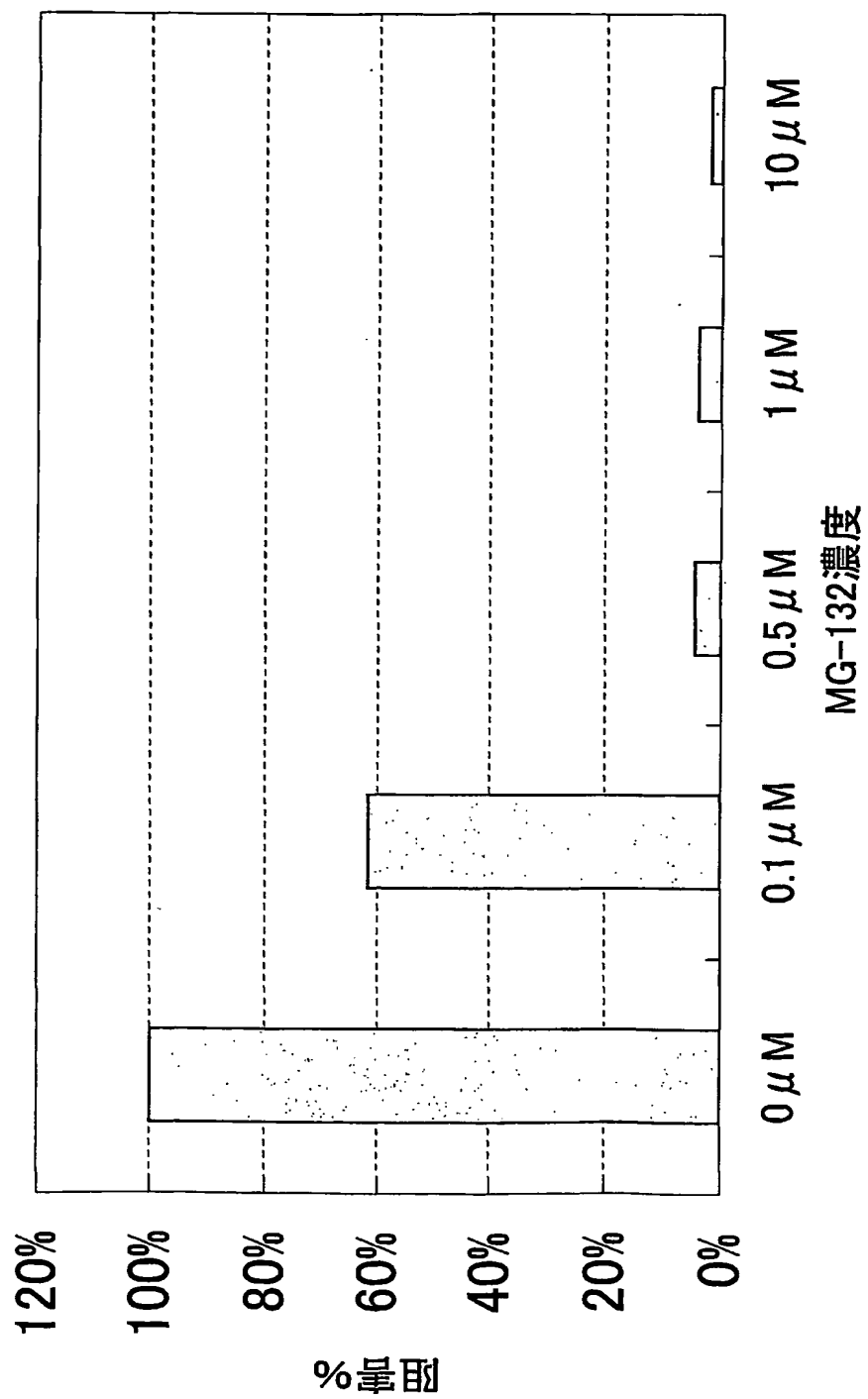


図20

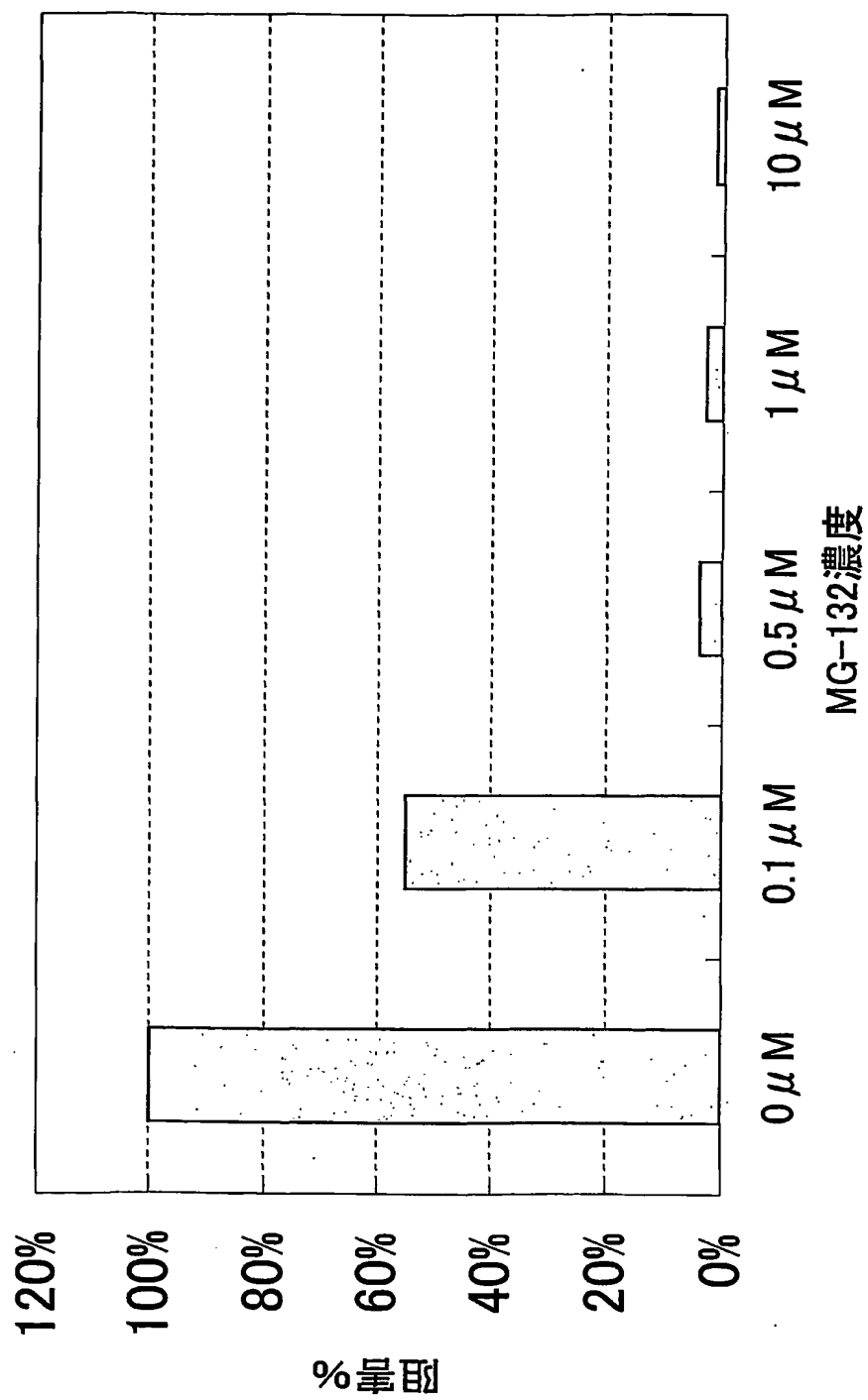


図21

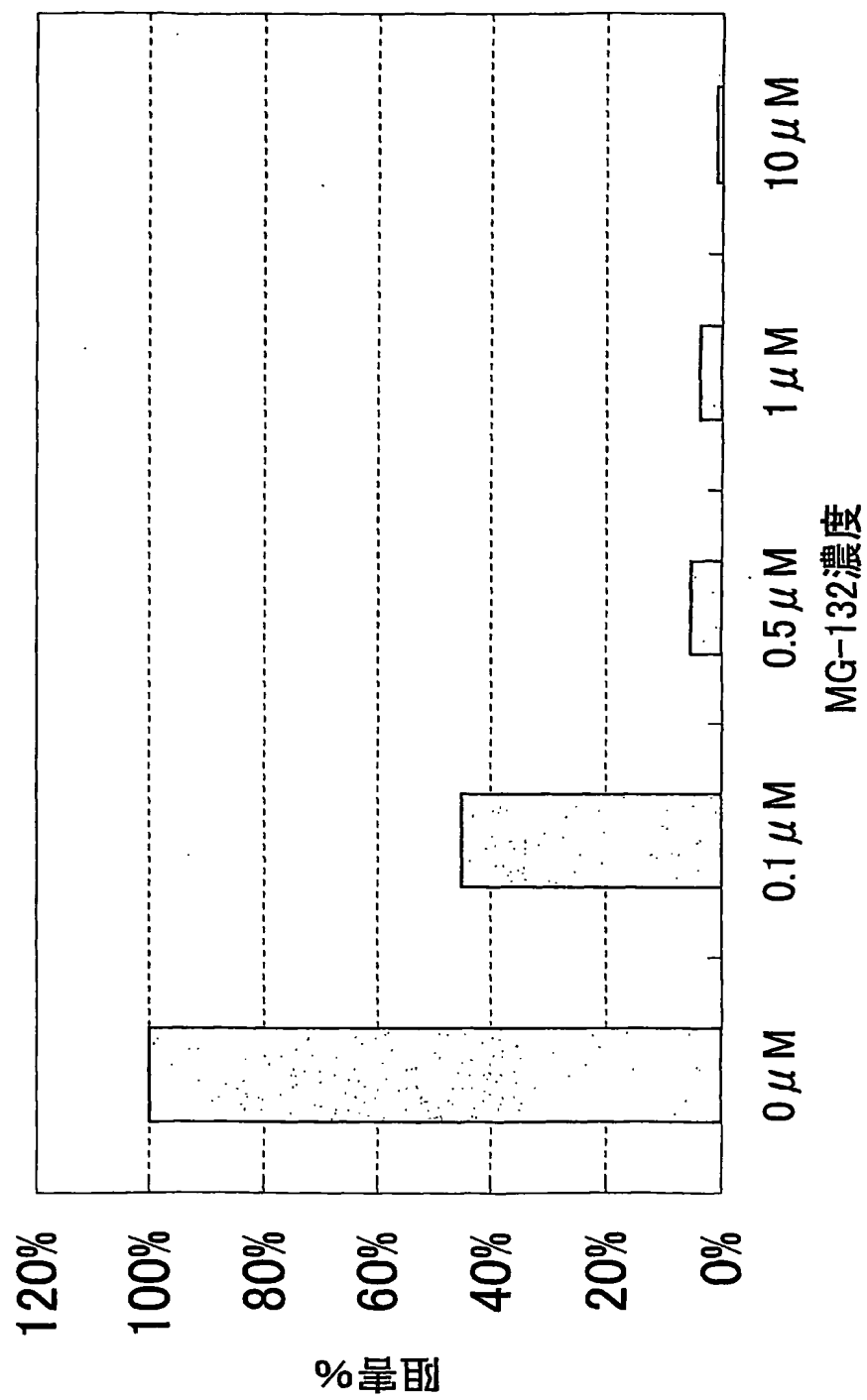


図22

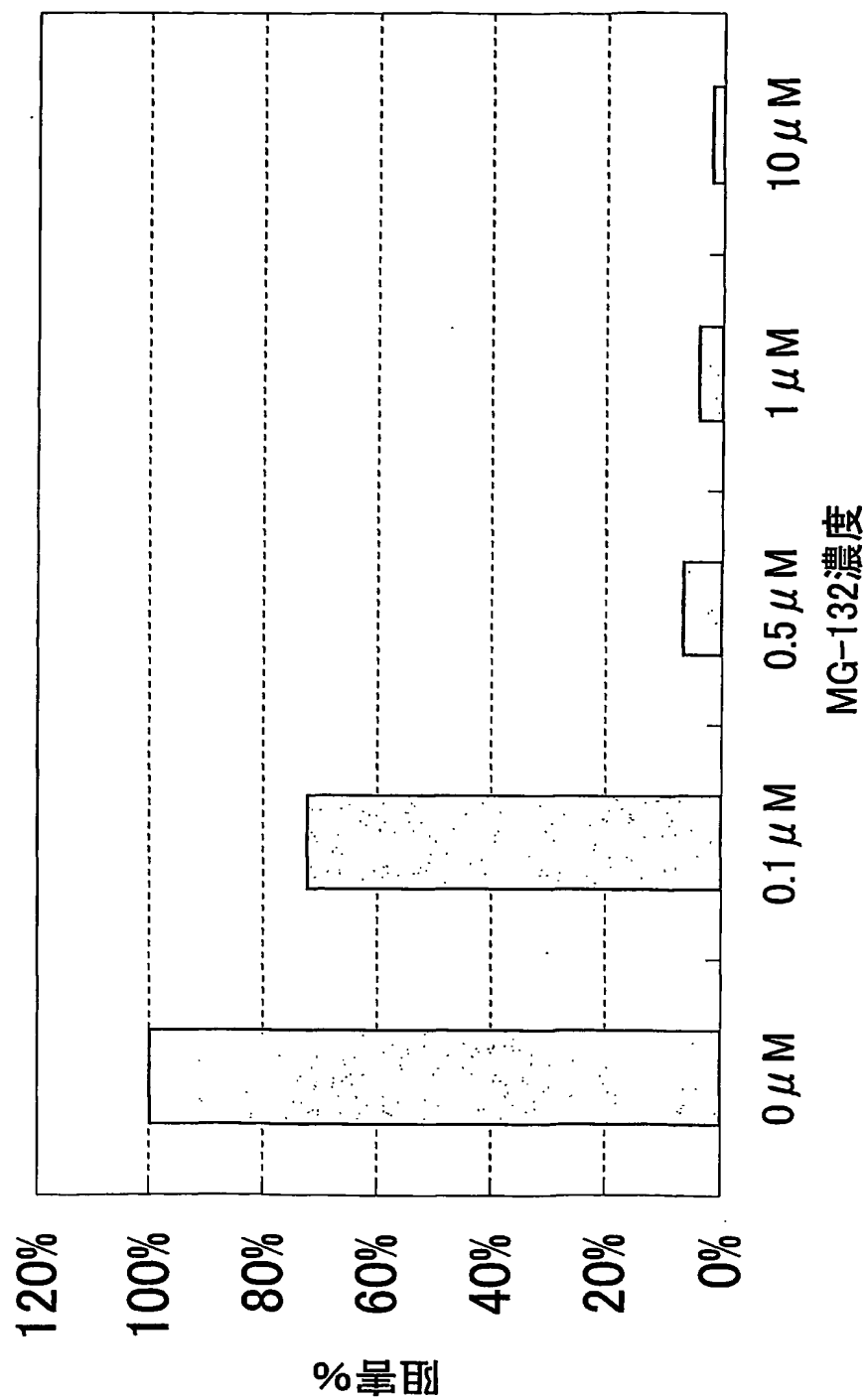


図23

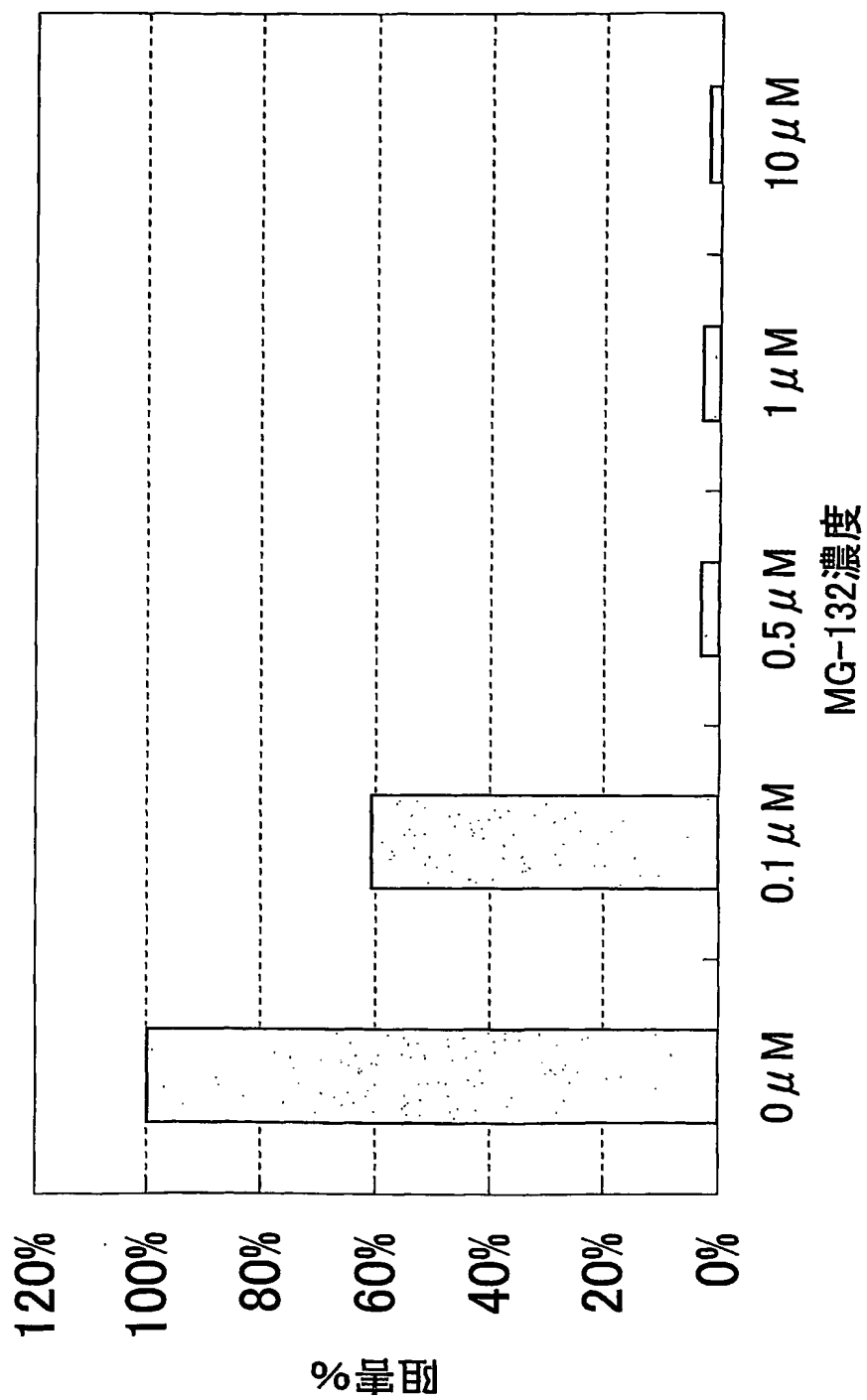


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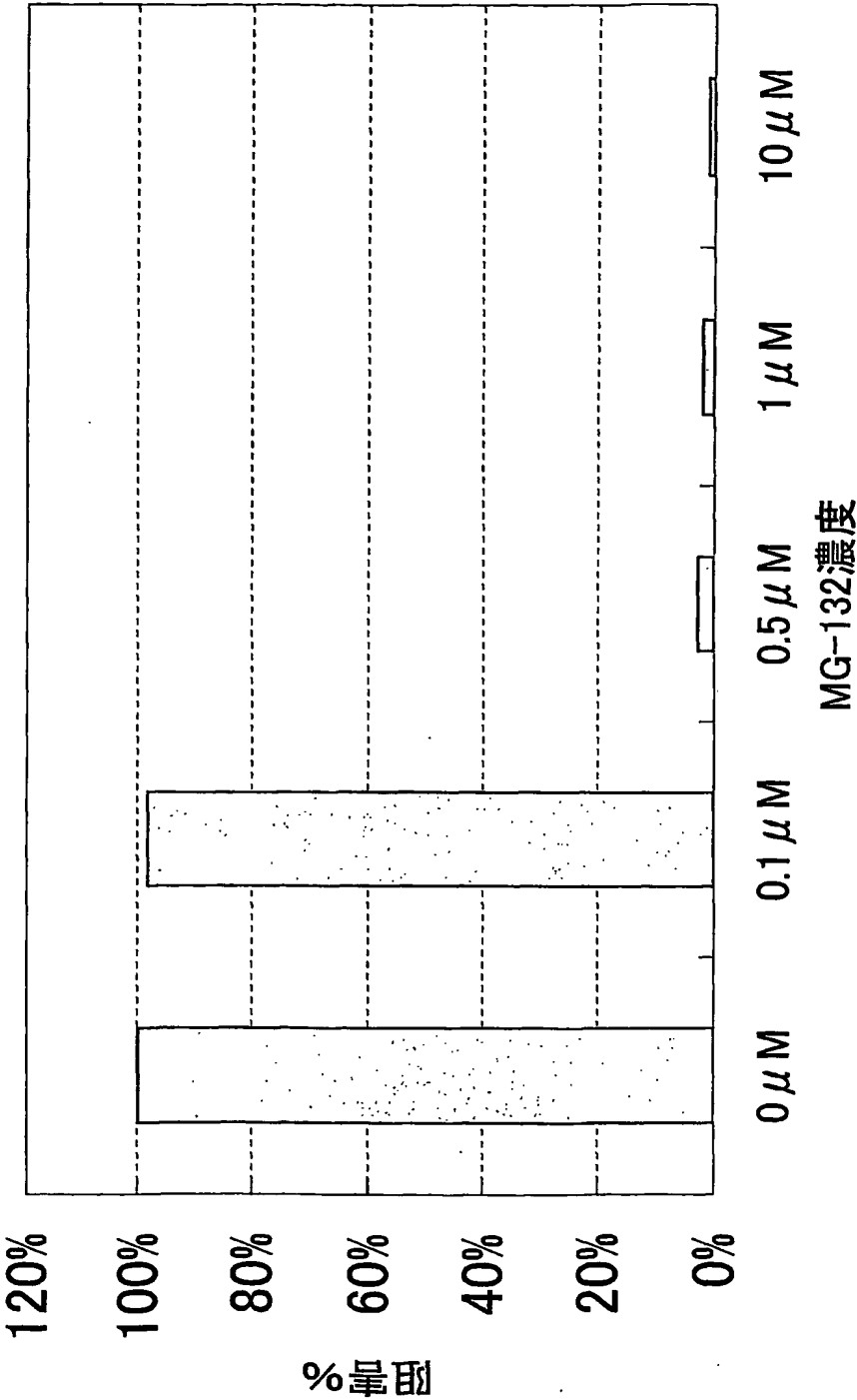


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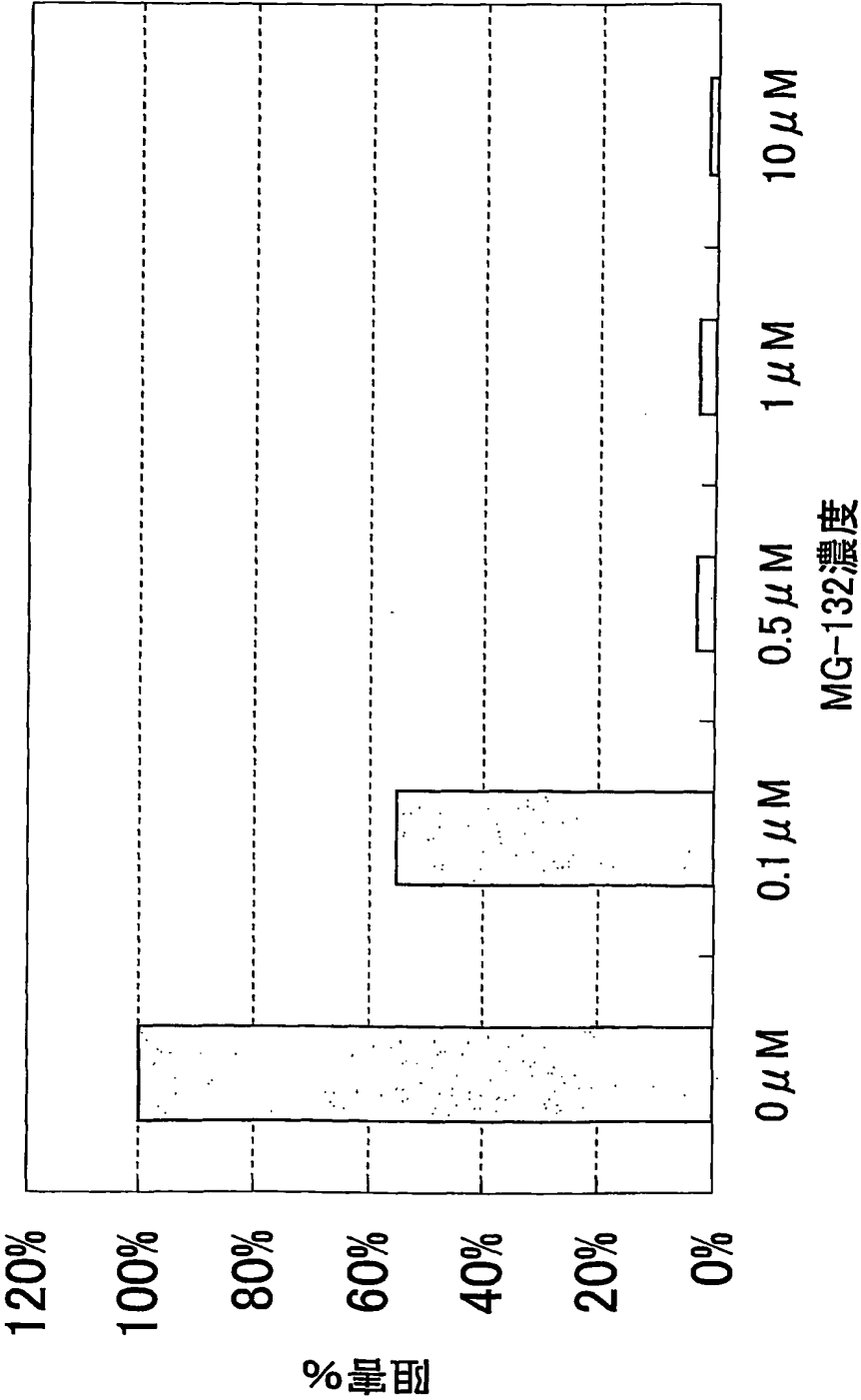


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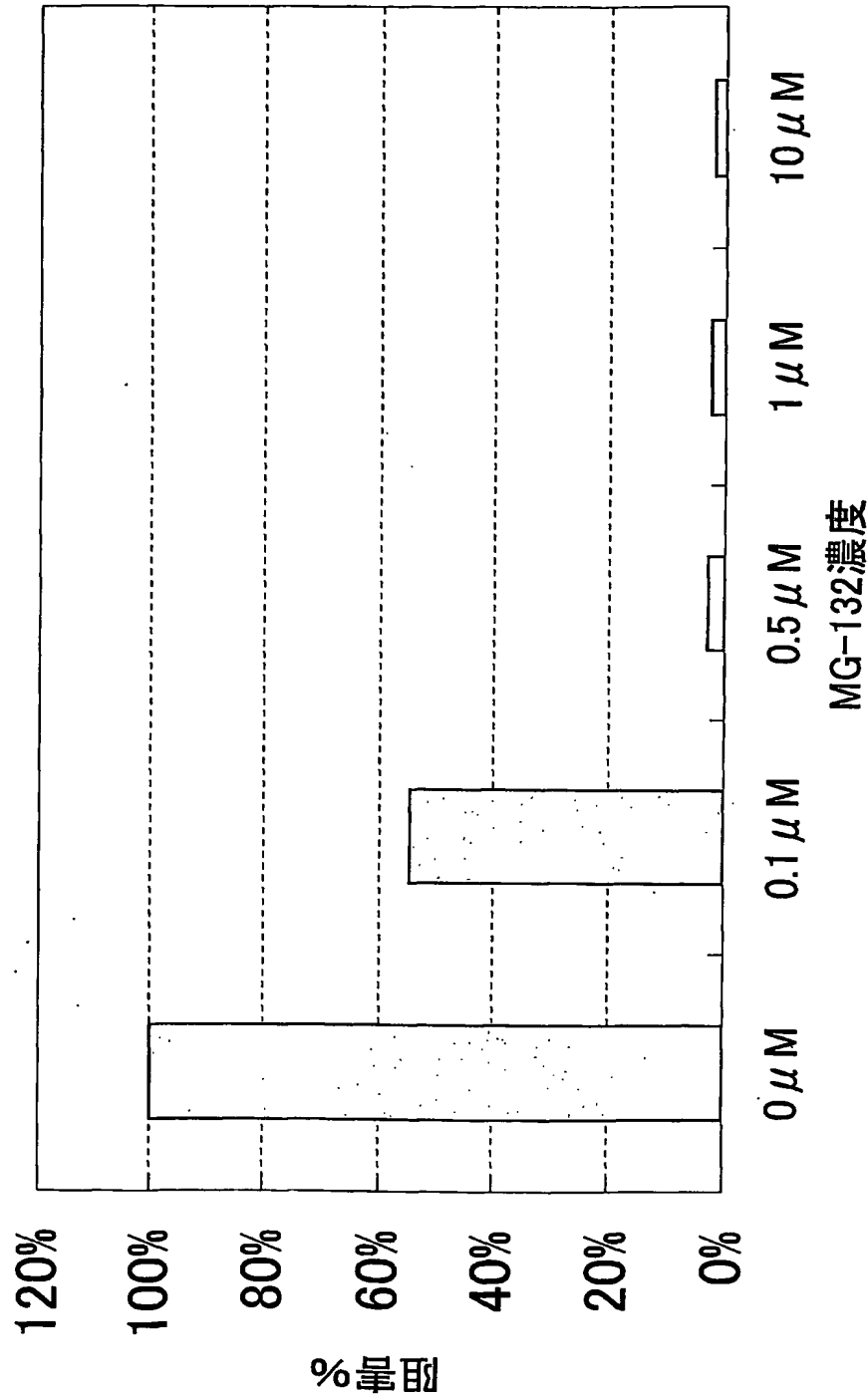


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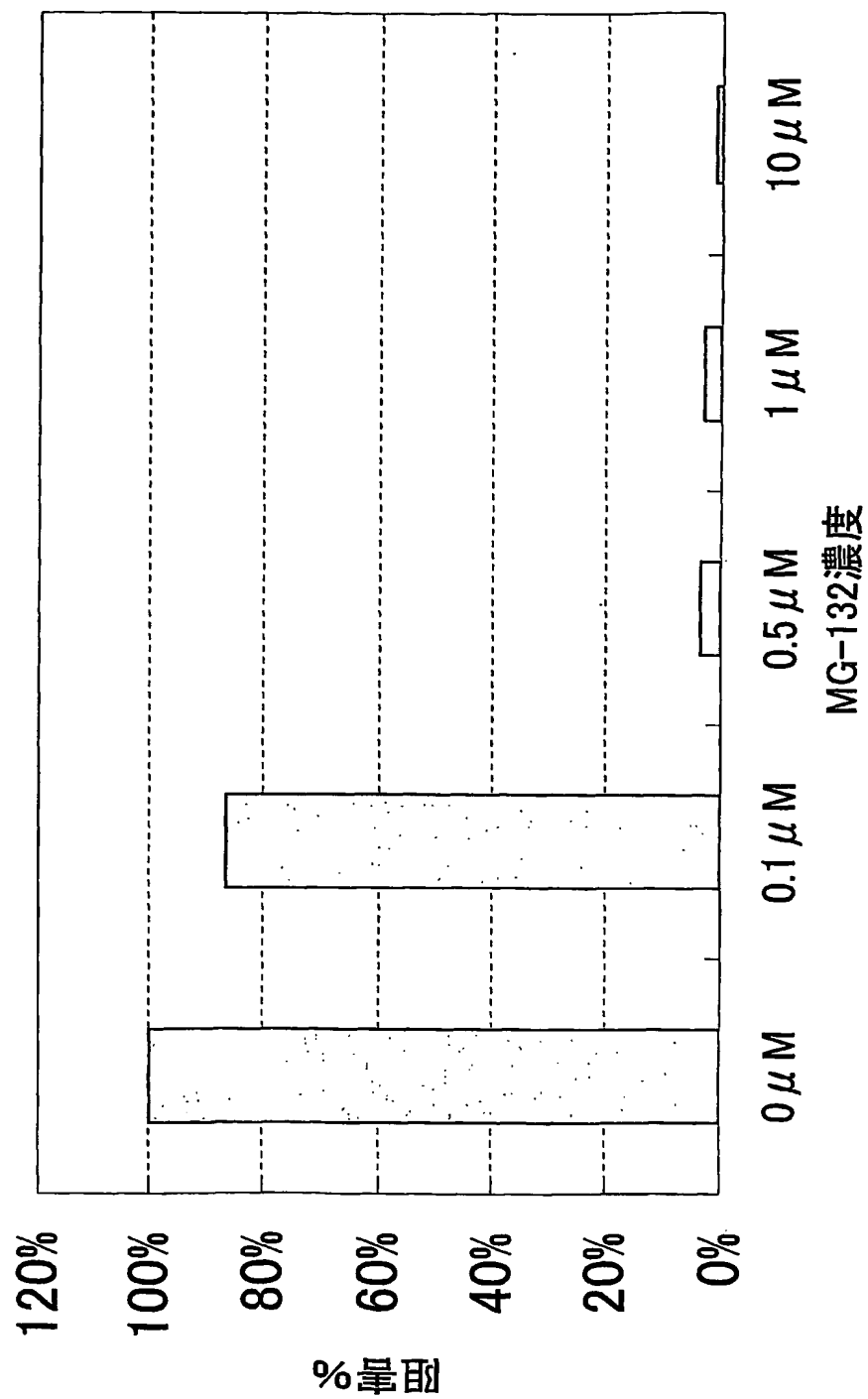


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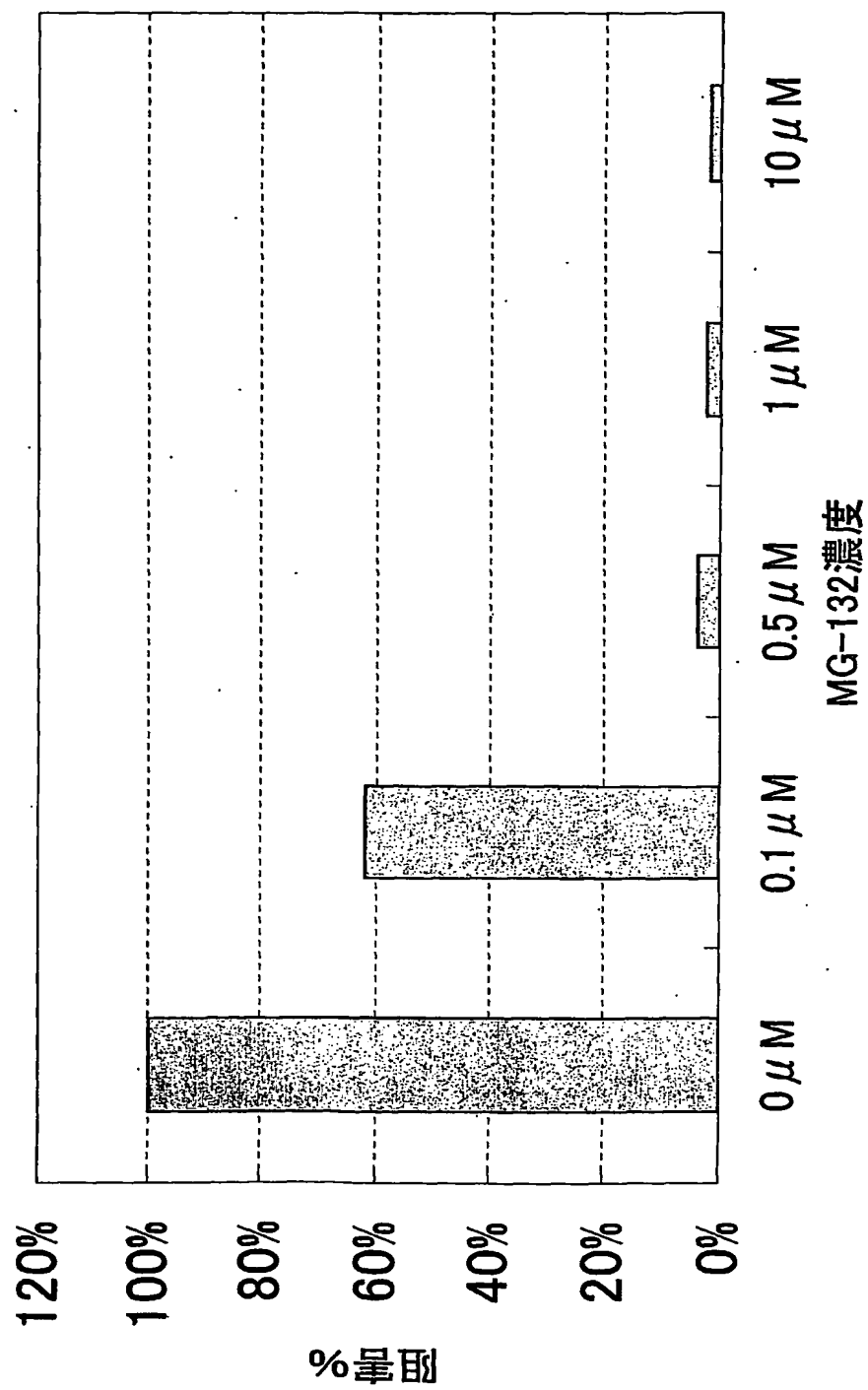
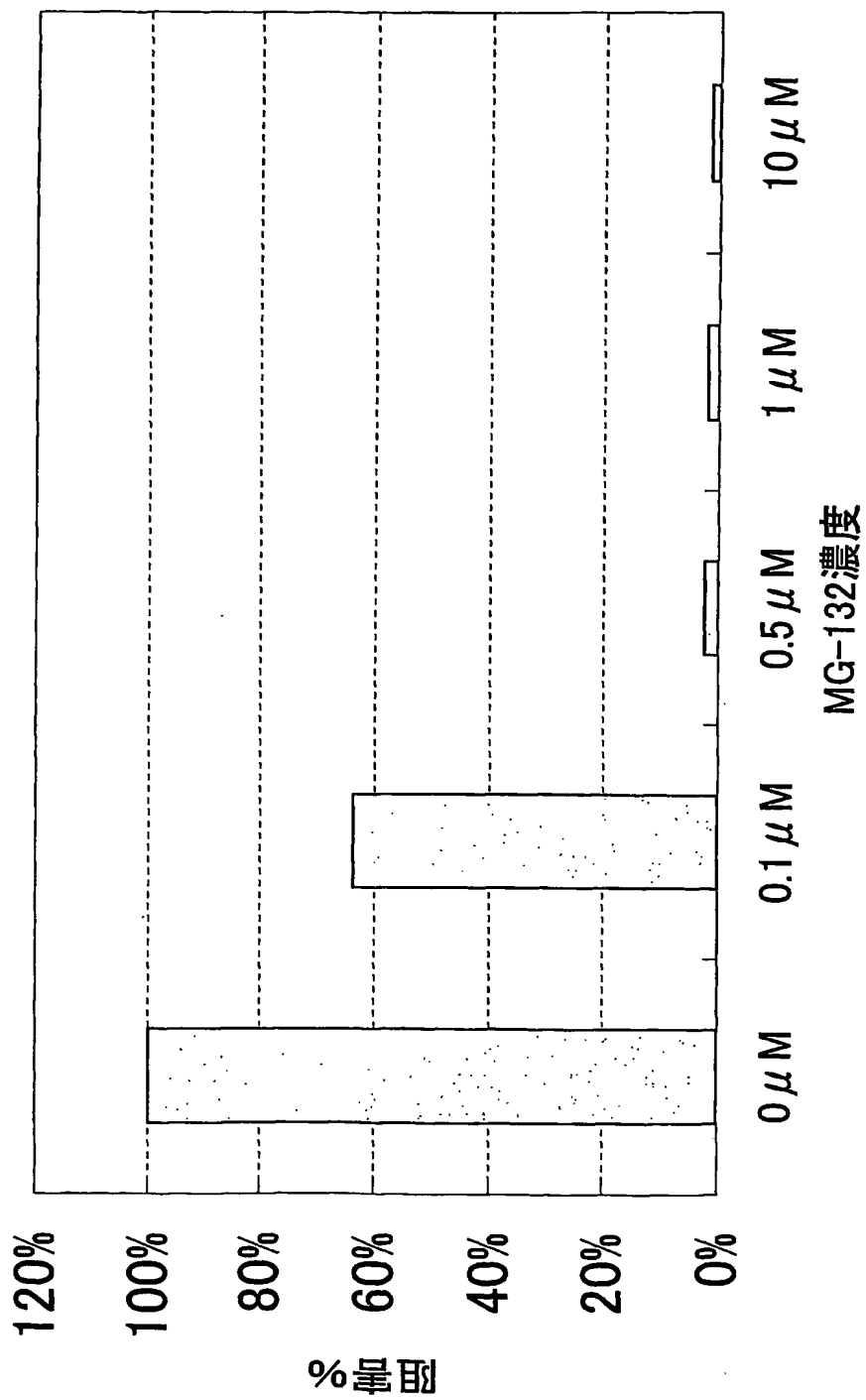


図29



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Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser

35 40 45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln

50 55 60

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly

65 70 75 80

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly

85 90 95

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr

100 105 110

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro

2/735

115

120

125

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser

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135

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Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser												
15				20					25			
cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325												
Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg												
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ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc 373												
Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe												
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Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp												
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110 115 120

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Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
125 130 135 140

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Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
145 150 155

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Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35 40 45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50 55 60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val

65 70 75 80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

85 90 95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val

100 105 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly

115 120 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln

130 135 140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp

145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu

165 170 175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu

180 185 190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro

195 200 205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro

210 215 220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225 230 235 240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245 250 255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
260 265 270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
275 280 285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
290 295 300

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Met

1

gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165

Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly

5

10

15

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Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp

20

25

30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261

Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr

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gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309

Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys

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tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
70 75 80

cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
85 90 95

aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
100 105 110

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Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
115 120 125

tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549
Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
130 135 140 145

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Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
150 155 160

tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
165 170 175

acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693

Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe

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185

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Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro

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Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro

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gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885

Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu

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250

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aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933

Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu

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Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser

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gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
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310 315 320

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Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
325 330 335

aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt 1181
Arg Arg

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Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50 55 60

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Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

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att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5 10 15 20

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Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40 45 50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70 75 80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85 90 95 100

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Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

105

110

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Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

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gtaaaaatgg taatagt

702

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<212> PRT

<213> Homo sapiens

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20

25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35

40

45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

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Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
115 120 125

Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
130 135 140

Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
145 150 155 160

Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
165 170 175

Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly
180 185 190

Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser
195 200 205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr
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Pro Ser Gly Met Val Phe His Arg Val
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aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

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Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

18/735

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Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp				
40	45	50		
gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc				428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro				
55	60	65		
aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa				476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu				
70	75	80		
att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac				524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His				
85	90	95	100	
atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg				572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu				
105	110	115		
gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc				620
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val				
120	125	130		

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Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp

135

140

145

act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc 716

Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe

150

155

160

aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat 764

Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp

165

170

175

180

gtc ctt cct tac gcc cag cat ctt cat cat tat ggt gtg gta ttg gag 812

Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu

185

190

195

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Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His

200

205

210

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Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met

215

220

225

gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttggtga catccgacag 963

Val Phe His Arg Val

230

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tgccagagag agctcaatgt acaaatgaat gcctcatggc tcttagctgt ggtttcttgg 1803

accagcggca tggacatttg tcagtttgcc ttctgacggt agcttttgga ggaagattcc 1863

tgcagccact aatgcattgt gtatgataac aaaaactctg gtatgacaca ttttctgtga 1923

tcattgttaa ttagtgacat agtaacatct gtagcagctg gtagtaaac ctcatgtggg 1983

ggtgggggtg ggtgtattc cttgggggat ggtttgggcc gaatggggag tggaatattt 2043

gacatttttc ctgttttaaa ttctaggata gattttaaca tcctttgcgg tcccagtcca 2103

aggtaggctg gtgtcatagt cttctcactc ctaatccatg accactgttt ttttcctatt 2163

tatatcacca ggtagccac tgagttaata tttaagttgt caatagataa gtgtccctgt 2223

tttgtggcat aatataactg aatttcatga gaagatttat tccaccaggg gtatttcagc 2283

tttgaaacca aatctgtgta tctaatacta accaatctgt tggatgtggg ttttaaaaaa 2343

tgtttgctaa actaccaag taagatttac tgtattaaat ggccttcggg tctgaaaagc 2403

tttttt 2409

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<211> 198

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu Ser

1 5 10 15
Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp
 20 25 30
Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
 35 40 45
Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
 50 55 60
Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
65 70 75 80
Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
 85 90 95
Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
 100 105 110
Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
 115 120 125
Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp
 130 135 140
Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
145 150 155 160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln

165

170

175

Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp

180

185

190

Arg His Val Val Leu Ser

195

<210> 10

<211> 1498

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86).. (679)

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ctgtgggacc gctgggcccc cagcg atg gcg acc ctg tgg gga ggc ctt ctt 112

Met Ala Thr Leu Trp Gly Gly Leu Leu

1

5

cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160

Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu

10

15

20

25

ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208
 Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg
 30 35 40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256
 Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr
 45 50 55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304
 Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu
 60 65 70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352
 Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys
 75 80 85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att 400
 Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
 90 95 100 105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr
 110 115 120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496
 Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala
 125 130 135

cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca 544

Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala

140

145

150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg 592

Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu

155

160

165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag 640

Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu

170

175

180

185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa 689

Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser

190

195

ttgaattcaa ggtgactaga aagaacagg cagacaactg gaaagaactg actgggtttt 749

gctgggtttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact 809

ggaagcaaaa acttgcttga tttttttttc ttgttaacgt aataatagag acatttttaa 869

aagcacacag ctcaaagtca gccataaagt cttttcctat ttgtgacttt tactaataaa 929

aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctctttttc 989

accacatagt tttaacttga ctttcaagat aattttcagg gtttttggtg ttgttggttt 1049

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tgcacccatg aacaaactgg ccatttgcta gtttactcta aagactaaac atagtcttgg 1409

tgtgtgtggt cttactcatc ttctagtacc ttttaaggaca aatcctaagg acttggacac 1469

ttgcaataaa gaaattttat tttaaaccc 1498

<210> 11

<211> 221

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

1 5 10 15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

20 25 30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

27/735

35 40 45
Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
50 55 60
Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
65 70 75 80
Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu
85 90 95
Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile
100 105 110
Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe
115 120 125
Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala
130 135 140
Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp
145 150 155 160
Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly
165 170 175
Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe
180 185 190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

210

215

220

<210> 12

<211> 1864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153).. (815)

<400> 12

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cccctcggcc tcccagcgct cccaagccgc agcggccgcg ccccttcagc tagctcgctc 120

gctcgctctg ctccccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg 173

Met Ala Leu Ala Leu Ala Ala

1

5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221

Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln

10

15

20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269

Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro

25

30

35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317

Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr

40

45

50

55

aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365

Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

60

65

70

aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413

Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr

75

80

85

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat 461

Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp

90

95

100

ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg 509

Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met

105

110

115

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557

Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu

120

125

130

135

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605

30/735

Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser

140

145

150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653

Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser

155

160

165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701

Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val

170

175

180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749

Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr

185

190

195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797

Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr

200

205

210

215

aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg 845

Arg Val Leu Phe Ile Tyr

220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtga tcaagatgca 905

gaacacagag gaataatcac ctgctttaaa aaaataaagt actgttgaaa agatcatttc 965

tctctatttg ttcttaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025

atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat 1085

gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145

ggggcagctt tgctttattc atcctccatc tcaaaatgaa cttggaatta aatattgtaa 1205

gatatgtata atgctggcca ttttaaaggg gttttctcaa aagttaaact tttgctatga 1265

ctgtgttttt gcacataatc catatttgct gtccaagtta atctagaaat ttattcaatt 1325

ctgtatgaac acctggaagc aaaatcatag tgcaaaaata catttaaggt gtggtcaaaa 1385

ataagtcttt aattggtaaa taataagcat taatttttta tagcctgtat tcacaattct 1445

gcggtacctt attgtaccta agggattcta aagggtttgt cactgtataa aacagaaagc 1505

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agcgttcttc acccccaccc ccacccccac ccccttatt ttctttttgt ctcctggtga 1625

ttaggccaaa gtctgggagt aaggagagga ttaggtactt aggagcaaag aaagaagtag 1685

cttgaactt ttgagatgat ccctaacata ctgtactact tgcttttaca atgtgttagc 1745

agaaaccagt gggttataat gtagaatgat gtgctttctg cccaagtggc aattcatctt 1805

ggtttgctat gttaaaactg taaatacaac agaacattaa taaatatctc ttgtgtagc 1864

<210> 13

<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln

100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115 120 125

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Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe

130

135

140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile

145

150

155

160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu

165

170

175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr

180

185

190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu

195

200

205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg

210

215

220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe

225

230

235

240

Leu Leu

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13).. (738)

<400> 14

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

1

5

10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15

20

25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30

35

40

45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50

55

60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243

Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65

70

75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291

Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

35/735

80	85	90	
gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339			
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu			
95	100	105	
aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387			
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe			
110	115	120	125
agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435			
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu			
	130	135	140
gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483			
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser			
145	150	155	
ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531			
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly			
160	165	170	
ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579			
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp			
175	180	185	
tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627			
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe			
190	195	200	205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675

Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210

215

220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723

Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

225

230

235

tat ttc ttc tta ttg tagagactgc atcaaccga cattcctttc ttataccaat 778

Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc ttttaagtatc tatatttcac ttgttttgca catatgcata 958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa 1138

ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198

atgaaacatc ttttgttata tagggtgtat tgaaacctgc agtgctgatt attagaaagg 1258

atttgtcaga ttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa 1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatatitta gaaacgtgag tgtaaagat agaatttggt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc cttataaga aaaataaatt ttattttaag 1558

ggacatacta gtttaggga tttcagatg ggaagctgca ttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtcttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg cttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttoggtta tatcttttgt tttgaatacc aacatttaaa atgatgggtat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158

cttattttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218

catttccaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278

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<210> 15

<211> 242

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85

90

95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln

100

105

110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115

120

125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe

130

135

140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile

145

150

155

160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu

165

170

175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr

180

185

190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu

195

200

205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg

210

215

220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe

225

230

235

240

Leu Leu

<210> 16

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13).. (738)

<400> 16

gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

1

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ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15

20

25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala

30

35

40

45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

41/735

50	55	60	
gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat			243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr			
65	70	75	
ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat			291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp			
80	85	90	
gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa			339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu			
95	100	105	
aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc			387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe			
110	115	120	125
agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg			435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu			
130	135	140	
gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc			483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser			
145	150	155	
ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga			531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly			
160	165	170	

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190 195 200 205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
210 215 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
225 230 235

tat ttc ttc tta ttg tagagactgc atcaaccoga cattcctttc ttataccaat 778
Tyr Phe Phe Leu Leu
240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc ttttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

tcttccagct tgtaaagcc attgacttct gacctgacat ttagtataat aaaaatgaaa 1138

ttcttaacca tgcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198

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attgtcaga ttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa 1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatatata 1438

cacacacata tatatatatta gaaacgtgag tgtaaagat agaatttggt ttaggacaaa 1498

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aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

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gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

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<210> 17

<211> 336

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

1 5 10 15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

45/735

35 40 45
Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
50 55 60
Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65 70 75 80
Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
85 90 95
His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
100 105 110
Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
115 120 125
Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr
130 135 140
Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145 150 155 160
Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
165 170 175
Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
180 185 190

Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile

195

200

205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln

210

215

220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala

225

230

235

240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn

245

250

255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu

260

265

270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr

275

280

285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu

290

295

300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met

305

310

315

320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335

<210> 18

47/735

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 18

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Met Ala

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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70

75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn

100

105

110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro

115

120

125

130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490
Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser

135

140

145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser

150

155

160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser

165

170

175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634

Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala

180

185

190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682

Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu

195

200

205

210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730

Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg

215

220

225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778

Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile

230

235

240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826

Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile

245

250

255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874

Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys

260

265

270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922

Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn

275

280

285

290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970

Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu

295 300 305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310 315 320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325 330 335

tagagactgc atcaaccgga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

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gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttcagct tgtaaatgcc 1420

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actaaatata tatgtgtata tgtatacaca tatatatata cacacacata tatatatTTa 1780

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actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560

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acagttttgt ttgct 2636

<210> 19

<211> 336

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

1 5 10 15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp

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85	90	95
His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu		
100	105	110
Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro		
115	120	125
Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr		
130	135	140
Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr		
145	150	155
Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro		
165	170	175
Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala		
180	185	190
Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile		
195	200	205
Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln		
210	215	220
Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala		
225	230	235
		240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn

245

250

255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu

260

265

270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr

275

280

285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu

290

295

300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met

305

310

315

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Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335

<210> 20

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53).. (1060)

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Met Ala

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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106

Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298

Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70

75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346

Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394

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Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490
 Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
 165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
 Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
 180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682
 Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
 195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
 Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
 57/735

215	220	225	
gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778			
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile			
230	235	240	
ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826			
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile			
245	250	255	
gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874			
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys			
260	265	270	
tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922			
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn			
275	280	285	290
gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970			
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu			
295	300	305	
ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018			
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu			
310	315	320	
agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060			
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu			
325	330	335	

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actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560

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<210> 21

<211> 76

<212> PRT

<213> Homo sapiens

<400> 21

Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr

1 5 10 15

Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val

20 25 30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn

35 40 45

Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr

50 55 60

Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

65 70 75

<210> 22

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (176)..(403)

<400> 22

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cggcctccgc ggtgcctgcc ttgcctctca ggttgaggag ctcaagcttg ggaaa atg 178

Met

1

gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa 226

Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys

5

10

15

aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274

Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser

20

25

30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322

Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys

35

40

45

ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370

Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys

50

55

60

65

gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg 423

Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

70

75

accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg 483

acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gataactaatc 543

aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaatga cctcattcct 603

aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt 663

aatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatctttgg 723

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tggagtacaa tttgtttgtg aaacagtcca gtgaaactgt gcagggaaat gaaggtagaa 843

ttttgggagg taataatgat gtgaaacata aagatttaat aattactgtc caacacagtg 903

gagcagcttg tccacaaata tagtaattac tatttattgc tctaaggaag attaaaaaaa 963

gatagggaaa agggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtctaatt 1023

tataaaatth taatccttac tgcatttctt ctgttctac aaatgtatta aacattcagt 1083

tt 1085

<210> 23

<211> 84

<212> PRT

<213> Homo sapiens

<400> 23

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
1 5 10 15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
50 55 60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
65 70 75 80

Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(316)

<400> 24

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cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

1

5

10

15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157

Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys

20

25

30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205

Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln

35

40

45

att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253

Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

50

55

60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301

Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His

65

70

75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356

Ser Leu Ser Gly Leu

80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggcttttagac 416

65/735

attggtggga ccaaggatgt ttgcaggat gccctgatcc taagaagggg gcctgggggt 476

gcgtgcagcc tgcggggag accccactct gtgcacctat tggctcttct agctgactct 536

tctcgttggg cttagagtct gcctgtttct gctagctccg tgtttagtcc acttgggtca 596

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gcacgcaagt gagcagacac caccgacttc ctttctgcgt caccagtgtc gtcagcagag 896

agaggacagc acaggctcaa ggttggtagt gaagtcaggt tcgggggtgca tgggctgtgg 956

tggtggtgat cagttgctcc agtgtttgaa ataagaagac tcatgtttat gtctggaata 1016

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aggaatgctt ggcctctggc aggcaggcag ctgtacccaa gctgggtggc agggggctgg 1376

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ggccctgcaa ggccacact cagccctgt gggatgatgt cacggtgggt ggggtggggc 1496

tgacccagc ttccagggga ctgtcactgt ggacgcaaa atggcataac tgagataagg 1556

tgaataagtg acaaataaag ccagtttttt acaaggt 1593

<210> 25

<211> 179

<212> PRT

<213> Homo sapiens

<400> 25

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu

1 5 10 15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val

20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala

67/735

50 55 60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
65 70 75 80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
85 90 95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
100 105 110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly
115 120 125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
130 135 140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr
145 150 155 160

Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala
165 170 175

Leu Leu Phe

<210> 26

<211> 1820

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114).. (650)

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acgcggagca gagctgagct gaagcggggac ccggagcccg agcagccgcc gcc atg 116

Met

1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164

Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

5

10

15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212

Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu

20

25

30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260

Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro

35

40

45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308

Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val

50

55

60

65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg 356
Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr
70 75 80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg 404
Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu
85 90 95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc 452
Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val
100 105 110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg 500
His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu
115 120 125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg 548
Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly
130 135 140 145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt 596
Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe
150 155 160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg 644
Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu
165 170 175

ctc ttc tgagcccgtc tcccggacag gttgaggaag ctgctccaga agcgcctcgg 700

Leu Phe

aaggggagct ctcatcatgg cgctgtctgc tgcggcatat ggacttttaa taatgttttt 760

gaatttcgta ttctttcatt ccactgtgta aagtgctaga cattttccaa tttaaaattt 820

tgctttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttattc agccgactgc 880

cagagaagtg ggaatggtat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc 940

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aatttctcac tctggttga agcacaacaa ctgaaatgtc tacgtttcat tttggcagta 1060

gggtgtgaag ctgggagcag atcatgtatt tcccggagac atgggacatt gctggcatgt 1120

ctccttcaca atcaggcgtg ggaatatctg gcttaggact gtttctctct aagacacat 1180

tgttttccct tattttaaaa gtgatttttt taaggacaga acttcttcca aaagagaggg 1240

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gaccaaggga caagaaggga cttgcctaaa gccaccacag aactcagcag cagaaccaag 1360

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ctagaccacag tcctgagcag gggagaggct cttgagacct gatgccctcc taccacatg 1480

gtttctccac tgccctgtct gctctgctgc tacaragggg cagggcctcc ccagccac 1540

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ctggaaggca ccaggcctca ggaggagccc catagtcccg cctgcagcct gtaaccatcg 1660

gctgggccct gcaaggccca cactcacgcc ctgtgggtga tggtcacggt gggtaggtgg 1720

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aaggtgaata agtgacaaat aaagccagtt tttacaagg 1820

<210> 27

<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1

5

10

15

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20

25

30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35

40

45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

72/735

73/735

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
210 215 220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225 230 235 240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
245 250 255

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
260 265 270

Ile Ala Lys Val Lys Ala Asn
275

<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (955)

<400> 28

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tgctccctcc gagcgctccg ccgttgcccg cctggcccct acggagtcct tagccagg 118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166
 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1 5 10 15

ccc egg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
 20 25 30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262
 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60

tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc 358
 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80

ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg 406
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95

gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg 454
 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110

ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt 502

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe

115

120

125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat 550

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His

130

135

140

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg 598

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro

145

150

155

160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc 646

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165

170

175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa 694

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180

185

190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag 742

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195

200

205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc 790

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser

210

215

220

tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc 838

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly

225 230 235 240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc 886

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr

245 250 255

aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt 934

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly

260 265 270

att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgcccacc 985

Ile Ala Lys Val Lys Ala Asn

275

taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct 1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct cccacagct 1105

gctctacagg gaccacggct ttggttctc accacttcc cccgggcagc tccagggatg 1165

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cccctccctg ccttaaaact tgggagagga gcactcaggg ctggccccac aaagggtctc 1285

gtggcctttt tcctcacaca gaagaggtca gcaataatgt cactgtggac ccagtctcac 1345

tcctccaccc cacacactga agcagtagct tctggggcaa aggtcagggt gggcgggggc 1405

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ggaaacc

1472

<210> 29

<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1

5

10

15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20

25

30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35

40

45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50

55

60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65

70

75

80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

85

90

95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100

105

110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala

115

120

125

Tyr Met Asp Ala Pro Lys Ala Ala Leu

130

135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145)..(555)

<400> 30

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ggaaattgaa actgagtggc ccacgatggg aagaggggaa agcccagggg tacaggaggc 120

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171

Met Gly Phe Gly Ala Thr Leu Ala Val

1

5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219

79/735

Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe
 10 15 20 25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267
 Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
 30 35 40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315
 Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
 45 50 55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363
 Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
 60 65 70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411
 Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro
 75 80 85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc 459
 Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
 90 95 100 105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc 507
 Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
 110 115 120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555
 Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu
 80/735

125

130

135

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtgg 615

gtgcaggcgc ggttccttac gcccctatgtg tgctgtgtgt gtccaggcac ggttccttac 675

gcccctatgtg tgctgtgtgt gtcctgcctg tatatgtggc ttcctctgat gctgacaagg 735

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gtacacttgt ttataataaa tgcaatcggtt tgg 1788

<210> 31

<211> 118

<212> PRT

<213> Homo sapiens

<400> 31

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1 5 10 15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

82/735

35 40 45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50 55 60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65 70 75 80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

85 90 95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100 105 110

Glu Cys Pro Cys Gln Leu

115

<210> 32

<211> 1908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(444)

<400> 32

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83/735

ggaggcctct gggatgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114

Met Gly Phe Gly Ala Thr Leu Ala

1

5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162

Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys

10

15

20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210

Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg

25

30

35

40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258

Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr

45

50

55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306

Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln

60

65

70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354

Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr

75

80

85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402

Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro

90

95

100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444
Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu
105 110 115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggctctgc ccctttctgc ttgcctgcc ctcacacggc agcccacat 564

gctcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagcctc cttacaaccc ggcctacatg gatgcccga aggcggccct ctgagcattc 684

cctggcctct ctggctgcc cttggttatg ttgtgtgtg gcgtgagtgg tgtgcaggcg 744

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cctgagaggt gggggcctct ccagggcaca tctggagttc ttctccagct taccctaggg 1044

tgaccaagta gggcctgtca caccagggtg gcgcagcttt ctgtgtgatg cagatgtgtc 1104

ctggtttcgg cagcgtagcc agctgtgtgt tgaggccatg gctcgtcccc ggagttgggg 1164

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ctttgatcct ttgggcagat gtcccatgtc tccctggagc ctgtcatgcc tgttggggat 1284
caggcagcct cctgatgcca gaacacctca ggcagagccc tactcagctg tacctgtctg 1344
cctggactgt cccctgtccc cgcactctcc ctgggaccag ctggagggcc acatgcacac 1404
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gcttcccagc accagcctca tggaatatgc aacaactcct gtaccccagt ccacggtgtt 1704
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tggtatggcag ctctggccca gacatgaata cctcgtgttc ctctccctc tattactgtt 1824
tcaccagagc tgtcttagct caaatctgtt gtgtttctga gtctagggtc tgtacacttg 1884
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<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln
1 5 10 15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala
20 25 30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro
35 40 45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala
50 55 60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val
65 70 75 80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
85 90 95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
100 105 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
115 120 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly
130 135 140

87/735

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly

145 150 155 160

Ser Asp Gly Gly Tyr Thr Ile Trp

165

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (573)

<400> 34

ctccgaacag gaagaggacg aaaaaaataa ccgtccgcga cgccgagaca aaccggaccc 60

gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro

1 5 10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159

Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro

15 20 25 30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207

88/735

Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
 35 40 45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255
 Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
 50 55 60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303
 Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val
 65 70 75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351
 Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
 80 85 90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399
 Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
 95 100 105 110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447
 Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
 115 120 125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495
 Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
 130 135 140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543
 Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
 89/735

145 150 155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc 593
Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp

160 165

tgtgccggga aagacatcac ataccttcag cactttcac aatgtaactg ctttagtcat 653

attaacctga agttgcagtt tagacacatg ttgttgggt gtctttctgg tgcccaaact 713

ttcaggcact tttcaaattt aataaggaac catgtaatgg tagcagtacc tccctaaagc 773

atittgaggt aggggaggta tccattcata aaatgaatgt gggatgaagcc gccctaagga 833

ttttccttta atttctctgg agtaatactg taccatactg gtctttgctt ttagtaataa 893

aacatcaaat taggtttgga gggaactttg atcttcctaa gaattaaagt tgccaaatta 953

ttctgattgg tctttaatct cctttaagtc ttgatatat attacttggt ataatggaa 1013

cgcattagtt gtctgccttt tcctttccat cccttgcccc acccatccca tctccaaccc 1073

tagtcttcca tttcctcccg ccagtcctca ttgaatcaat ggtgcaggac agaaagccag 1133

tcagactaat ttccttcttt cctcgactt ctcccactc gtcactttt aactagtgtt 1193

tcacaaggat cctctgaaac cctctctgtg cccaagtac agatgccatt acttctgctt 1253

togtatctcc tcaggcaaaa gtggagggtg ccttatgggc cctcctcata ggttgtctct 1313

90/735

gcatacacga acctaaccga aatttgcttt ggtgccagaa aaactgagct atgtttgaac 1373

aaagatgtcg tgcaaactgt actgtgaaca acagttggtt taaaatatga ggggcaagga 1433

ggaggatgca tttcaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca 1493

gatcaaaaac tggttaccat ttttgtcag agtgtctgat gcggccactc attcggctcc 1553

ccagaattcc tagactgggt taatagggtc atattgtgaa tgtctcacta caaatgact 1613

tgagtccagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673

ttttgttttc tgaaattgga ttttatttta ttttatctta taatttcagt tcatctaaat 1733

tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcgtt 1793

gtatgtctct ctctacactg tgggtgcactt aacttgtgga atttttatac taaaaatgta 1853

gaataaagac tattttgaag atttgaataa agtgatgaag ttgc 1897

<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu

1 5 10 15
Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
 20 25 30
Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
 35 40 45
Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
 50 55 60
Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
65 70 75 80
Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
 85 90 95
Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe
 100 105 110
Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
 115 120 125
Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
 130 135 140
Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
145 150 155 160

Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr

165 170 175

Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg

180 185 190

Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala

195 200 205

Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro

210 215 220

Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly

225 230 235 240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu

245 250 255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys

260 265 270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe

275 280 285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala

290 295 300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr

305 310 315 320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val

325

330

335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile

340

345

350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr

355

360

365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala

370

375

380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met

385

390

395

400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu

405

410

415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val

420

425

430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala

435

440

445

Pro Glu Lys Gln Met Ala Pro

450

455

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1480)

<400> 36

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tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacct tcgcc atg 118

Met

1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166

Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe

5

10

15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214

Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr

20

25

30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262

Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala

35

40

45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310

95/735

Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val
50 55 60 65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358
Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val
70 75 80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406
Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe
85 90 95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454
Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser
100 105 110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502
Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp
115 120 125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
130 135 140 145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
150 155 160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646
Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe
96/735

165	170	175	
ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg			694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu			
180	185	190	
ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg			742
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met			
195	200	205	
gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca			790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser			
210	215	220	225
ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt			838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser			
230	235	240	
gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta			886
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu			
245	250	255	
agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag			934
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu			
260	265	270	
aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt			982
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu			
275	280	285	

ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc 1030
Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
290 295 300 305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga 1078
Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
310 315 320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag 1126
Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
325 330 335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc 1174
Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val
340 345 350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc 1222
Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala
355 360 365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag 1270
Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln
370 375 380 385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt 1318
Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser
390 395 400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366

Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu

405

410

415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414

Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser

420

425

430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462

Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro

435

440

445

gag aag caa atg gca cct tgaacttaag cctactacag actgtagag 1510

Glu Lys Gln Met Ala Pro

450

455

gccagtgggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570

ttataaaca acaaaatgct atggtagcat ttttcacctt catagcatac tccttccccg 1630

tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagaggagg aactaactca 1690

agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750

agccaagaaa ctaaagggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgtagga tttccgtttt aagggtcaca tggaagagg tatagctttg 1870

ccttgagatt gactcattaa aatcagagac tgt 1903

99/735

<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser

1 5 10 15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala

20 25 30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser

35 40 45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile

50 55 60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser

65 70 75 80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met

85 90 95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala

100 105 110

100/735

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
115 120 125

Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu
130 135 140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu
145 150 155 160

Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val
165 170 175

Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp
180 185 190

Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe
195 200 205

Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
210 215 220

Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
225 230 235 240

Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
245 250 255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
260 265 270
101/735

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His

275

280

285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser

290

295

300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp

305

310

315

320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292)..(1257)

<400> 38

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tcggagagcc gagtgaagac atttcacct ggacacctga ccatgtgcct gccctgagca 180

102/735

gcgaggccca ccaggcatct ctgttggtggg cagcagggcc aggtcctggt ctgtggaccc 240

tcggcagttg gcaggctccc tctgcagtgg ggtctggggc tcggccccac c atg tcg 297

Met Ser

1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc 345

Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser

5

10

15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca 393

Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala

20

25

30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca 441

Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala

35

40

45

50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt 489

Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser

55

60

65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac 537

Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr

70

75

80

tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc 585

Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly

103/735

85	90	95	
gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg			633
Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu			
100	105	110	
ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc			681
Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser			
115	120	125	130
aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc			729
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser			
	135	140	145
aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg			777
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu			
150	155	160	
cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag			825
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu			
165	170	175	
cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag			873
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu			
180	185	190	
gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac			921
Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr			
195	200	205	210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca 969
Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
215 220 225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag 1017
Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu
230 235 240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag 1065
Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
245 250 255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac 1113
Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
260 265 270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161
Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile
275 280 285 290

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct 1209
Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
295 300 305

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag 1257
Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
310 315 320

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377

tcacagattt cattcctggt tttatatata tattttttgt tgcgtttta acatctccac 1437

gtccctagca t 1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn

1 5 10 15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His

20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu

35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys

50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu

65 70 75 80

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Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu

85

90

95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe

100

105

110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly

115

120

125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile

130

135

140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val

145

150

155

160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala

165

170

175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly

180

185

190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val

195

200

205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr

210

215

220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met

107/735

225 230 235 240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser

 245 250 255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu

 260 265 270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro

 275 280 285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys

 290 295 300

Gln Met His Ile Trp Met Ser Ser Thr

305 310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(1091)

<400> 40

ggcgggaaccg agctgacggg cgtgcggccg ctgcgccgca aactcgtgtg ggacgcaccg 60
108/735

ctccagccgc ccgcgggcca ggcacccggt cccccagcgg cagccgagcc cgcccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173

Met Ala Gly Gln Pro Gly His

1

5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221

Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro

10

15

20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269

Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg

25

30

35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317

Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln

40

45

50

55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365

Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val

60

65

70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413

Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg

75

80

85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461

Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro

109/735

90	95	100	
aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac			509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn			
105	110	115	
att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag			557
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys			
120	125	130	135
tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag			605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys			
140	145	150	
tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg			653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg			
155	160	165	
gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg			701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr			
170	175	180	
ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct			749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser			
185	190	195	
gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca			797
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser			
200	205	210	215

ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg 845

Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp

220

225

230

tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc 893

Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe

235

240

245

tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag 941

Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln

250

255

260

tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga 989

Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg

265

270

275

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037

Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp

280

285

290

295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085

Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser

300

305

310

agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac ttgccttac 1141

Ser Thr

ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201

tcagcagggtt ccccaaaagg ctgcccagcc ttacagcaga tgctgaaggc agagcagctg 1261

agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

gttggtggaca atctcagctg ggtcaataag ggcagggtggc tcagcgagcc acggcagccc 1381

cctgtatctg gattgtaatg tgaatcttta gggtaattcc tccagtgacc tgtcaaggct 1441

tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501

ttagtaccgg gttcagttta gttcttggta tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro

1 5 10 15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr

20 25 30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln

112/735

35 40 45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
50 55 60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
65 70 75 80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
85 90 95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
100 105 110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
115 120 125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
130 135 140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
145 150 155 160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
165 170 175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
180 185 190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
195 200 205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
210 215 220

Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225 230 235 240

Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
245 250 255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
260 265 270

Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
275 280 285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
290 295 300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305 310 315 320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
325 330 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
340 345 350
114/735

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg

355

360

365

Ala Lys Glu

370

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(1203)

<400> 42

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ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114

Met Ser His Glu Lys Ser Phe Leu

1

5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162

Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly

10

15

20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210

115/735

Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala
 25 30 35 40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258
 Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly
 45 50 55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306
 Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly
 60 65 70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354
 Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly
 75 80 85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402
 Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr
 90 95 100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450
 Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe
 105 110 115 120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag 498
 Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu
 125 130 135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546
 Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp
 116/735

140	145	150	
gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg 594			
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val			
155	160	165	
ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act 642			
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr			
170	175	180	
ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac 690			
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr			
185	190	195	200
tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt 738			
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys			
205	210	215	
tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg 786			
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser			
220	225	230	
gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc 834			
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe			
235	240	245	
tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc 882			
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val			
250	255	260	

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930

Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr

265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978

Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe

285 290 295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026

Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr

300 305 310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074

Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr

315 320 325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122

Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr

330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170

Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu

345 350 355 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223

Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu

365 370

gtgcccgtc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283
tacttcccct ctctcttgtc ccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343
ctcctgtatg tacactgcag atacttccat ttggaccgc tgtggccaca gcatggcccc 1403
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gtccccggga gagggattga gccaagaggt gaggtgcac gtcttcctc ctgtcccagc 1583
tccccagcct ggcgtagagc acccctcccc tccccccac cccctggag tgctgcctc 1643
tggggacatg cggagtgggg gtcttatccc tgtctgagc cctgaggga gagaggatgg 1703
catgtttcag gggaggggga agccttcctc tcaatttgtt gtcagtgaat ttccaataaa 1763
tgggatttgc tctctgcc 1781

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

1

5

10

15

119/735

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20

25

30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35

40

45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50

55

60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65

70

75

80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85

90

95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100

105

110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115

120

125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130

135

140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala

145

150

155

160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala

120/735

165	170	175
Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val		
180	185	190
Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu		
195	200	205
Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser		
210	215	220
Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr		
225	230	235
240		
His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly		
245	250	255
Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly		
260	265	270
Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala		
275	280	285
Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr		
290	295	300
Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn		
305	310	315
320		

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu

325

330

335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340

345

350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355

360

365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370

375

380

Leu Val Pro Gly Pro Glu Lys Glu Asn

385

390

<210> 44

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 44

agctgtgcac tctccatcca gctgtgcgct ctgctggga gtcccagcc atg tcc gac 58

Met Ser Asp

1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
 Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
 5 10 15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
 Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
 20 25 30 35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta 202
 Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
 40 45 50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
 Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
 55 60 65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298
 Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
 70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
 Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
 85 90 95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394
 Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
 100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly

120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val

135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe

150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val

165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His

180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr

200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu

215 220 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778

124/735

Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230

235

240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826

Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245

250

255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874

Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu

260

265

270

275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922

Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu

280

285

290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970

Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn

295

300

305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018

Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val

310

315

320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066

Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser

325

330

335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114

Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys

125/735

340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met

360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro

375 380 385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac 1258
Gly Pro Glu Lys Glu Asn

390

cagcgaaggg agaagttggg aagctacgtt ctgttgcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct cctcccccg aagtctctg tggatgac cgctctccc 1378

tgccctccc cgcttctga cctctgaaga ggttggaag tgaccatttg gatgtctggg 1438

ccctgccaag gcgacagga ggtcagagg gaggcggct gcttcctgcc cccaccctt 1498

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tgtgctttca cctctgcctc atcttctc ccgtccctgc ccgcccact cccaaagaa 1618

ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctt 1678

ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttcca 1738

126/735

atctcgtcct ctgtcccaaa ctctttaagc acaattgggc ttcttccatc tccaggtttt 1798

ctgccattct taaccaaggc agccccaagc ctcttgggga ggcagggcaa aaacaggtgc 1858

cctcatcgtg gtctgtgcca tgtcccgtct ctatggtggt tgaggagaaa ggcggggaag 1918

cttcctcagc ctgacagata tgtgtggcat ttactagcca gagctctgaa aggcagtgc 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038

gaggccctac tgccttctca aagcagagag gcagcttatc aaactcagcc caaaactctg 2098

tttcatggg tggggagatg gagcaggga gtacagagtg ggatggtcag gacctgggcc 2158

attgcaacca aaatggggac ttcttgggta gggaggtcac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaccatt gcaatgggag gtggaggga aggctcagcc 2278

tcctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

1 5 10 15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20 25 30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala

128/735

145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala

 165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val

 180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu

 195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser

 210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr

225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly

 245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly

 260 265 270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala

 275 280 285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr

290 295 300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn

305 310 315 320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu

325 330 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340 345 350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355 360 365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370 375 380

Leu Val Pro Gly Pro Glu Lys Gln Asn

385 390

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<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 46

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Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70

75

80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346

Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85

90

95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394

131/735

Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
 100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
 Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
 120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
 Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
 135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
 Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
 150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
 Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
 165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
 Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
 180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
 Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
 200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
 Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
 132/735

215	220	225	
gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778			
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr			
230	235	240	
gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826			
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile			
245	250	255	
gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874			
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu			
260	265	270	275
ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922			
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu			
280	285	290	
acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970			
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn			
295	300	305	
cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018			
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val			
310	315	320	
tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066			
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser			
325	330	335	

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ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
375 380 385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258
Gly Pro Glu Lys Gln Asn
390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct ccctcccccg aagttctctg tggatgatgac cgctctcccc 1378

tgccctccc cgcttcctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438

ccctgccaag gcgacagga gggtcagagg gaggcggct gcttcctgcc cccaccctt 1498

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ggattaggga gggttattgc cccaaccatt gcaatgggag gtggaggagc aggctcagcc 2278

tcctcattgt ctaaagtagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

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<210> 47

<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly

1 5 10 15

Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys

20 25 30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe

35 40 45

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys

50 55 60

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile

65 70 75 80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu

85 90 95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val

100 105 110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val

115 120 125

Asp Lys Val Gly Glu Ser Asn Asn Met Val

136/735

130

135

<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

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<222> (110).. (523)

<400> 48

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Met Ile Ser

1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166

Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val

5

10

15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214

Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu

20

25

30

35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262

Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly

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40 45 50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct 310
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala
55 60 65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358
Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro
70 75 80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg
85 90 95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu
100 105 110 115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
120 125 130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553
Gly Glu Ser Asn Asn Met Val
135

aaatattgtg ttatttataa agtcatttga agaatttca gcacaaaatt aaattacatg 613

aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673
138/735

caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc ttgaaggcta 793

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tgcatgatg taatttttct ttcttcttc ttttttttaa attttagcag tggcttatta 1453

ttgtttttc ataaattaa ataatgttta cttaagaca tgtaacatgt 1513

taaaaggta aacttatggc tgtttttaaa gggctattca tttaatctga gttttccctt 1573

attttcagct ttttcctagc atataatagt cattaagcat gacatatcct tcatatgac 1633

actcatcttg agttaattag aaaataacctg agttcacgtg ctaaagtcac ttcactgtaa 1693

taaactgact atggtttctt aagaacatga cactaaaaaa aaagtgggtt tttccaccg 1753

ttgctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

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tgaatttcta tcaaaatggt ctttgactg taacagagat tccttttttc aataatctta 2473

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gagagaggct ggagcagttt tcagttttaa atgagtcctgc agttaatatc aaatgtgagt 2593

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cagccttctg tctgtaacaa aaatgtactt tatagagatg gaggaaaagg tctaatacta 2773

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gaatgttttt cttttccctt tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893

cccactgtca gattatatta tctaacaatt gaatattgta aatatacttg tcttacctct 2953

caataaaaagg gtacttttct att 2976

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe
141/735

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His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln
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Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val
35 40 45
Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro
50 55 60
Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
65 70 75 80
Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
85 90 95
Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser
100 105 110
Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
115 120 125
His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
130 135 140
Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
145 150 155 160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His

165

170

175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr

180

185

190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu

195

200

205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro

210

215

220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile

225

230

235

240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser

245

250

255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser

260

265

270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe

275

280

285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His

290

295

300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met

305

310

315

320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser

325

330

335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser

340

345

350

Arg Ser Thr Thr His Leu Ile

355

<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (327)..(1403)

<400> 50

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aacgtggttg acctatcctt gcaccagagg agattaagac tatttttggt agcatcccag 180

atatctttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240

atgagagcaa aagcattggt gacatTTTTc tgaaatattc aaaagatttg gtaaaaacct 300

acctccctt tgtaaacttc ttgaa atg agc aag gaa aca att att aaa tgt 353

Met Ser Lys Glu Thr Ile Ile Lys Cys

1

5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401

Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala

10

15

20

25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449

Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro

30

35

40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497

Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys

45

50

55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545

His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile

60

65

70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593

Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys

75

80

85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641

Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly

90

95

100

105

145/735

tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt 689
Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val
110 115 120

gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta 737
Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val
125 130 135

act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac 785
Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His
140 145 150

aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca 833
Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro
155 160 165

gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag 881
Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys
170 175 180 185

gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg 929
Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu
190 195 200

ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag 977
Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln
205 210 215

atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt 1025

Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys

220

225

230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att 1073

Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile

235

240

245

tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac 1121

Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp

250

255

260

265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag 1169

Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys

270

275

280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga 1217

Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg

285

290

295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265

Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser

300

305

310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta 1313

Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu

315

320

325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa 1361

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Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu

330

335

340

345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata 1403

Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

350

355

tgaagcgta ccaaaatctt aaattataga aatgtataga cacctcatatc tcaaataaga 1463

aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523

cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583

caagttaatt catgtaaaaa atgatatgta ttttgatgta atttatctct tgtttgaatc 1643

tgtcattcaa aggccaataa ttttaagttgc tatcagctga tattagtagc tttgcaaccc 1703

tgatagagta aataaatttt atgggcgggt gccaaatact gctgtgaatc tatttgtata 1763

gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagatta 1823

aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883

ttcacatgtg cagtttgaag tatttaaata accactcctt tcacagtta ttttcttctc 1943

aagcgttttc aagatctagc atgtggattt taaaagattt gccctcatta acaagaataa 2003

catttaaagg agattgtttc aaaatatatt tgcaaattga gataaggaca gaaagattga 2063

gaaacattgt atattttgca aaaacaagat gttttagct gtttcagaga gactacggt 2123

tatttatggt aattttatcc actagcaaact ctgtatttag ttgatagtg tgtggaattt 2183

tattttgaag gataagacca tgggaaaatt gtggtaaaga ctgtttgtac cttcatgaa 2243

ataattctga agttgccatc agttttacta atcttctgtg aaatgcatag atatgcgc 2303

gttcaacttt ttattgtggt cttataatta aatgtaaaat tgaaaattca ttgctgttt 2363

caaagtgtga tatctttcac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423

catatggata aatgcatttt tatttcctat ttctttagg agtgctacaa atgtttgtca 2483

cttaaatttc aagtttctgt tttaatagtt aactgactat agattgtttt ctatgcatg 2543

tatgtgccac ttctgagagt agtaaagac tctttgtac attttaaaag caattgtatt 2603

agtaagaact ttgtaaataa atacctaaaa ccc 2636

<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu

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15

149/735

Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu

20

25

30

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln

35

40

45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu

50

55

60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu

65

70

75

80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val

85

90

95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys

100

105

110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln

115

120

125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser

130

135

140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu

145

150

155

160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg

150/735

165 170 175
Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
180 185 190
Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
195 200 205
Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
210 215 220
Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
225 230 235 240
Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
245 250 255
Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu
260 265 270
Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys
275 280 285
Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu
290 295 300
Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met
305 310 315 320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
325 330 335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu
340 345 350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe
355 360 365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
370 375 380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
385 390 395 400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro
405 410 415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
420 425 430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
435 440 445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
450 455 460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
465 470 475 480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp

485

490

495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu

500

505

510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu

515

520

525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu

530

535

540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu

545

550

555

560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu

565

570

575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr

580

585

590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn

595

600

605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val

610

615

620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser

153/735

625 630 635 640
Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp
 645 650 655
Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile
 660 665 670
Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
 675 680 685
Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
 690 695 700
Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
705 710 715 720
Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val
 725 730 735
Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp
 740 745 750
Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp
 755 760 765
Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn
 770 775 780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys
785 790 795 800

Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro
805 810 815

Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu
820 825 830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser
835 840 845

Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu
850 855 860

Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr
865 870 875 880

His Leu Ile

<210> 52

<211> 3910

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (29).. (2677)

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Met Ala Glu Asn Ser Val Leu Thr

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5

tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct 100

Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser

10

15

20

aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca 148

Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser

25

30

35

40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt 196

Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val

45

50

55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244

Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile

60

65

70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg 292

Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu

75

80

85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat 340

Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp

156/735

90	95	100	
tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca	388		
Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro			
105	110	115	120
cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca	436		
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser			
125	130	135	
tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt	484		
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe			
140	145	150	
act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc	532		
Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val			
155	160	165	
cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca	580		
His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr			
170	175	180	
cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg	628		
His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val			
185	190	195	200
agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg	676		
Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp			
205	210	215	
157/735			

gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga 724

Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg

220

225

230

aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg 772

Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu

235

240

245

gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg 820

Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met

250

255

260

caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt 868

Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu

265

270

275

280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag 916

Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys

285

290

295

aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg 964

Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met

300

305

310

gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act 1012

Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr

315

320

325

cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac 1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn

330

335

340

agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca 1108
Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser

345

350

355

360

aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct 1156
Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala

365

370

375

gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca 1204
Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro

380

385

390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct 1252
Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser

395

400

405

tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa 1300
Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln

410

415

420

gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg 1348
Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu

425

430

435

440

gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa 1396

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Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln

445

450

455

cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt 1444

Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly

460

465

470

agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt 1492

Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu

475

480

485

gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att 1540

Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile

490

495

500

ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta 1588

Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val

505

510

515

520

aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag 1636

Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln

525

530

535

aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa 1684

Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu

540

545

550

tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg 1732

Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg

160/735

555	560	565	
tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct	1780		
Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala			
570	575	580	
gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg	1828		
Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu			
585	590	595	600
aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct	1876		
Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala			
605	610	615	
caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct	1924		
Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala			
620	625	630	
aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att	1972		
Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile			
635	640	645	
tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc	2020		
Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe			
650	655	660	
ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att	2068		
Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile			
665	670	675	680

ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt 2116
Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu
685 690 695

aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac 2164
Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp
700 705 710

ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg 2212
Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg
715 720 725

cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca 2260
Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser
730 735 740

gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta 2308
Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val
745 750 755 760

gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct 2356
Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala
765 770 775

gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg 2404
Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu
780 785 790

agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga 2452

Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg

795

800

805

gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt 2500

Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu

810

815

820

atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat 2548

Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp

825

830

835

840

aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc 2596

Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile

845

850

855

cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt 2644

Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser

860

865

870

cat acg tta agt aga tct aca act cat ttg ata tgaagcgta ccaaaatctt 2697

His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

875

880

aaattataga aatgtataga cacctcatac tcaaataaga aactgactta aatggtactt 2757

gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817

ttttcttct tgaaagagta aggtttacct gttacatddd caagttaatt catgtaaaaa 2877

163/735

atgatagtga ttttgatgta atttatctct tgtttgaatc tgcattcaa aggccaataa 2937

ttaaagttgc tatcagctga tattagtagc ttgcaaccc tgatagagta aataaatttt 2997

atgggcggtt gccaaatact gctgtgaatc tatttgtata gtatccatga atgaatttat 3057

ggaaatagat atttgtgcag ctcaatttat gcagagatta aatgacatca taatactgga 3117

tgaaaacttg catagaattc tgattaaata gtgggtctgt ttcacatgtg cagtttgaag 3177

tatttaaata accactcctt tcacagttaa tttcttctc aagcgttttc aagatctagc 3237

atgtggattt taaaagattt gccctcatta acaagaataa catttaaagg agattgtttc 3297

aaaatatttt tgcaaattga gataaggaca gaaagattga gaaacattgt atattttgca 3357

aaaacaagat gttttagct gtttcagaga gactacggtt tatttatggt aattttatcc 3417

actagcaaat ctgatttag tttgatagtg tgtggaattt tattttgaag gataagacca 3477

tgggaaaatt gtggtaaaga ctgtttgtac cttcatgaa ataattctga agttgccatc 3537

agttttacta atcttctgtg aaatgcatag atatgcgat gttcaacttt ttattgtggt 3597

cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657

aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717

tatttcctat ttcttttagg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777

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atacctaataa ccc 3910

<210> 53

<211> 622

<212> PRT

<213> Homo sapiens

<400> 53

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Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn

20 25 30

Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser

35 40 45

Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg

50 55 60

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys

65 70 75 80

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Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp

85

90

95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly

100

105

110

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His

115

120

125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu

130

135

140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln

145

150

155

160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn

165

170

175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys

180

185

190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser

195

200

205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala

210

215

220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly

166/735

225 230 235 240

Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met
 245 250 255

Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu
 260 265 270

Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln
 275 280 285

Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp
 290 295 300

Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys
305 310 315 320

Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg
 325 330 335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu
 340 345 350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe
 355 360 365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile
 370 375 380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly
385 390 395 400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu
405 410 415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu
420 425 430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys
435 440 445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly
450 455 460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met
465 470 475 480

Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
485 490 495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
500 505 510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
515 520 525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
530 535 540

Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys

545 550 555 560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr

565 570 575

Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys

580 585 590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr

595 600 605

Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val

610 615 620

<210> 54

<211> 2426

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (104)..(1969)

<400> 54

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gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg 115

Met Glu Gly Pro

1

ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca 163

Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro

5

10

15

20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211

Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala

25

30

35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259

Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp

40

45

50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307

Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu

55

60

65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg 355

Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser

70

75

80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403

Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe

85

90

95

100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451

170/735

Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn

105

110

115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499

Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val

120

125

130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547

Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu

135

140

145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595

Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile

150

155

160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643

Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val

165

170

175

180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691

Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro

185

190

195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt 739

Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val

200

205

210

gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga 787

Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly

171/735

215	220	225	
aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat 835			
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp			
230	235	240	
atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac 883			
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn			
245	250	255	260
aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga 931			
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg			
265	270	275	
gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc 979			
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu			
280	285	290	
ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac 1027			
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr			
295	300	305	
ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta 1075			
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu			
310	315	320	
gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg 1123			
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly			
325	330	335	340

tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt 1171

Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val

345

350

355

ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca 1219

Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala

360

365

370

gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta 1267

Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu

375

380

385

tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct 1315

Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala

390

395

400

tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc 1363

Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly

405

410

415

420

tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca 1411

Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro

425

430

435

tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat 1459

Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr

440

445

450

gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat 1507
Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His

455

460

465

cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg 1555
His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp

470

475

480

att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca 1603
Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr

485

490

495

500

ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt 1651
Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys

505

510

515

tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca 1699
Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser

520

525

530

tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg 1747
Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu

535

540

545

ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat 1795
Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His

550

555

560

atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc 1843

174/735

Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe
565 570 575 580

atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg 1891
Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val
585 590 595

aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac 1939
Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His
600 605 610

cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa 1989
Pro Ala Arg Glu Lys Val Leu Arg Ser Val
615 620

ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaag tgaagtaaag 2049

atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa 2109

aagttctcaa taaaggcatt acaatttttt aggtttagaa agatggactt ttctgataaa 2169

tcttggcaga catctaaaaa aaaaaccata tttttcacia gaaaatgcaa gttacttttt 2229

ttggaaataa tactcactga ttatggataa aatggaatat tttcagatac tatattggct 2289

gtttcaaaat agtactattc tttaaacttg taatttttgc taagttattt gtctttgttg 2349

tatctataaa tatgtaaaaa atatttaaata agatgtacct gttttgcttt cacacttaat 2409

aaaaaatttt tttttgt

2426

<210> 55

<211> 257

<212> PRT

<213> Homo sapiens

<400> 55

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met

1 5 10 15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe

20 25 30

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro

35 40 45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu

50 55 60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu

65 70 75 80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly

85 90 95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg

100 105 110

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Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly

115

120

125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly

130

135

140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln

145

150

155

160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly

165

170

175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu

180

185

190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala

195

200

205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr

210

215

220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu

225

230

235

240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp

245

250

255

Gly

177/735

<210> 56

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10).. (780)

<400> 56

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Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu

1

5

10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99

Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly

15

20

25

30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147

Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg

35

40

45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195

Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala

50

55

60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243
Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe

65

70

75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291
Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr

80

85

90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339
Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr

95

100

105

110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387
Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly

115

120

125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc 435
Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser

130

135

140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca 483
Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser

145

150

155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca 531
Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro

160

165

170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg 579
179/735

Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu
 175 180 185 190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627
 Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile
 195 200 205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675
 Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val
 210 215 220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723
 Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys
 225 230 235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771
 Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala
 240 245 250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc 820
 Thr Asp Gly
 255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttatatt atgctttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgttgg gagggcagga gccctggcac taatgctgta 1000

caggtttttt tcctgttagg agagctgagg ccagctgcc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tgtttgaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg ccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca 1300

gggtatgcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttc 1420

tgctgtctct gtttctagct ccatggttgg cctggtgggg gtggagttcc ctcccaaaca 1480

ccagaccaca cagtcctcca aaaataaaca ttttatatag 1520

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln

1

5

10

15

Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys

181/735

20 25 30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu
35 40 45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
50 55 60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
65 70 75 80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
85 90 95

Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
100 105

<210> 58

<211> 1496

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9).. (329)

<400> 58

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182/735

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp
 1 5 10

atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98
 Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
 15 20 25 30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146
 Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
 35 40 45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194
 Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
 50 55 60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242
 Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp
 65 70 75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 290
 Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met
 80 85 90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc 339
 Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
 95 100 105

tttgatgac ccttcctttt tacctcattt atttggtact ttccccacac agtcctttat 399

ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459

caaaccattc agatcagcca ctgtctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaacca ggactcagtc 579

ctgcttcttt tgctcagat gattttcttc tgtttttcac taaataagca aatgaaaact 639

ctctccatta cttctgtctt tctctttgtc cacttacgca gtaggtgact ggcattgtgcc 699

acagagcagg cctgcctca ctgtctgtg gtcagttctg ggttcactta atggctttgt 759

gaatgtaaat aaggggcagg tcttgccct agaggattga gatgttttc tatatcttag 819

aactatTTTT ggataaatta tatatTTTcc ttcctagtag aagtgttact gcctgtaact 879

agctcaaaat accaatgcag tttctgcatt ctgggttttg tttttctttt tttttttttt 939

ttttttgagt tttgtcttg tcgcccaggc tggagtgcaa tggcgtgatc tcagctcact 999

ggcaacatct gcctcccggg ttcaaatgat tctctgcct cagtctcctg agtagctggg 1059

attacaggtg cccgccacca cgctcagcta atttttgtat ttttagtaga gatggggttt 1119

taccatgttg gccaggctgg tcttagactc ctgacctcag ttgatccacc tgcctcagcc 1179

tctgcattca gtttattcac atatTTTTgg taactcccat ggcagctcct aggatttcag 1239

cggctctgtg gccagaaagc aggcaccagg gctgacctca aggccgtatc agagggccaa 1299

gcagagttct tttggatacc tgcttttcat cccacagggc cttagagtca gaggtaaggt 1359

agcaacagag ctagaatggg gcaatgcact cttaccctcc ttctcaactt ttatttaagc 1419

tgtgctaaat gttttcttca agggaaccag atttagttct ttacagaatt ttccagtga 1479

ataaaacatg ttgtaat 1496

<210> 59

<211> 272

<212> PRT

<213> Homo sapiens

<400> 59

Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly

1 5 10 15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp

20 25 30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met

35 40 45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly

50 55 60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln

185/735

65	70	75	80
Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr	85	90	95
Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr	100	105	110
Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys	115	120	125
Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg	130	135	140
Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu	145	150	155
His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro	165	170	175
Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val	180	185	190
Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr	195	200	205
Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu	210	215	220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln
225 230 235 240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu
245 250 255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
260 265 270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117)..(932)

<400> 60

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gccgccgccg ctgcttcagc ttattccttg tggcctctgc gggctcctgcc tcagcc atg 119

Met

1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167

Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

5

10

15

187/735

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215

Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val

20

25

30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263

Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met

35

40

45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311

Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile

50

55

60

65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359

Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly

70

75

80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407

Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu

85

90

95

ggg gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455

Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr

100

105

110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503

Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val

115

120

125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551

Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu

130 135 140 145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599

Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His

150 155 160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647

Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser

165 170 175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu

180 185 190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743

Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr

195 200 205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791

Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met

210 215 220 225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839

His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr

230 235 240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887

189/735

Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg

245

250

255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa 932

Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

260

265

270

taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta 992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052

taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgtactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagtgagca 1232

cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292

aatcccaatg ccttgtgact ttcataggat tcttgatcat gcatgttgat gtactggctc 1352

ttcactttgg gctttctgat gtttattcac acctttggag agttgcaact tgccacatac 1412

gaaattagtc tcatagtgtg gtgaacttca accccaaaat tttaaaaatg tatttcccc 1472

cagttttaaa ttgccttga aatttaaaaa aaaaaattta gacttagtac cagaaccaa 1532

aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct 1592

gtgtgtgtgt gtgtgtgtgt gtgtatacag actttttttt ttaacttggt gattcagatg 1652

tcttgggtccc tgaatagtcc tagattactt attttgagaa ttgattgtta aaaattacag 1712

ggaattaaaa taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc 1772

tctgaaaatt ttattagttt attcttgtgg agaataccaa gaaaatgtgt atttccccat 1832

tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtcttt ttttaagagg 1892

agaataaaca ataaggaatt actg 1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser

1 5 10 15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp

20 25 30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln

35 40 45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

191/735

50 55 60
Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
65 70 75 80
Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile
85 90 95
Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly
100 105 110
Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile
115 120 125
Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu
130 135 140
Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu
145 150 155 160
Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala
165 170 175
Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile
180 185 190
Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val
195 200 205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser

210

215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49).. (705)

<400> 62

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Met Asn Arg

1

ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105

Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

5

10

15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153

Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile

20

25

30

35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201

Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys

40

45

50

193/735

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249

Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg

55

60

65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297

Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala

70

75

80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345

Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu

85

90

95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393

Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu

100

105

110

115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441

Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu

120

125

130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489

Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu

135

140

145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537

Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu

150

155

160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585
Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp

165

170

175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633
Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly

180

185

190

195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681
Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe

200

205

210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735
Gly Leu Pro Gln Ile Pro Ala Ser

215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat 795

ttaggtttct ttcctttctt tgaaggaaag tttaattaca ttgctctttt attttttcca 855

ttaagagact cattgcttgg gaaatgcttt ctctgtacta aaatttgatt cctttttttt 915

cttatgaaaa acgaactcag tttaaaagta ttttagctc gtaggacttg ttttcattca 975

ttaataataa ttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035

ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095

ttcatattat gattcagaat catittctat tgttggtatta taggttggtt aaagtgatgg 1155

195/735

cctttttgat gggttttggt gtgtcttggt aacaagtcgt tactgtgtcc attattggaa 1215

tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcagtatta 1275

catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt 1335

tatactcaat aaatattttt caaaagg 1362

<210> 63

<211> 622

<212> PRT

<213> Homo sapiens

<400> 63

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro

1 5 10 15

Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly

20 25 30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr

35 40 45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg

50 55 60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn

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65 70 75 80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val
 85 90 95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp
 100 105 110

Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser
 115 120 125

Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp
 130 135 140

Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr
145 150 155 160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met
 165 170 175

Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His
 180 185 190

Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn
 195 200 205

Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu
 210 215 220

Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn

225 230 235 240

Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys

245 250 255

Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln

260 265 270

Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp

275 280 285

Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile

290 295 300

Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile

305 310 315 320

Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser

325 330 335

Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile

340 345 350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe

355 360 365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn

370 375 380

Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
385 390 395 400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
405 410 415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
420 425 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
199/735

530 535 540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg
545 550 555 560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe
565 570 575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys
580 585 590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr
595 600 605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val
610 615 620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14).. (1879)

<400> 64

atttaacacc aag atg gcg gac ggc ccg gat gag tac gat acc gaa gcg 49
200/735

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala

1

5

10

ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97

Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His

15

20

25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145

Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp

30

35

40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat 193

Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr

45

50

55

60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg 241

Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro

65

70

75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga 289

Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg

80

85

90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa 337

Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln

95

100

105

ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa 385

Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln

201/735

110 115 120

ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct 433
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro
125 130 135 140

tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag 481
Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln
145 150 155

ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat 529
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp
160 165 170

gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca 577
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala
175 180 185

tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat 625
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn
190 195 200

gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat 673
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His
205 210 215 220

tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa 721
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu
225 230 235

202/735

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt 769

Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu

240

245

250

gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa 817

Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln

255

260

265

gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag 865

Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys

270

275

280

ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct 913

Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro

285

290

295

300

ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat 961

Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp

305

310

315

tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta 1009

Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val

320

325

330

cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg 1057

Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu

335

340

345

ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg 1105
Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp

350

355

360

ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca 1153
Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro

365

370

375

380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg 1201
Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp

385

390

395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag 1249
Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys

400

405

410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc 1297
Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe

415

420

425

tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt 1345
Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly

430

435

440

gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg 1393
Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val

445

450

455

460

ggc aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta 1441

Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu

465

470

475

ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct 1489

Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser

480

485

490

tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg 1537

Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp

495

500

505

aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg 1585

Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met

510

515

520

ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg 1633

Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met

525

530

535

540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga 1681

Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg

545

550

555

atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att 1729

Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile

560

565

570

gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt 1777

Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe

205/735

575 580 585

gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc 1825
Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr

590 595 600

agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag 1873
Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln

605 610 615 620

ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg cctgaaaatt 1929
Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tgtagggcta atgggtgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct cacagtattt 2169

ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat cagaaatgtt 2229

cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc agtctagtac 2289

gagtattgca tctaattcca ggagcattgt ttttaagttga ttgactagtt attatgtaca 2349

tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc tactgtgatg 2409

ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca atgttttggt 2469

tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529

tactctgagg ttttaagggtc tgataatgaa gcaattgcat gagtatagta agtcatgttt 2589

ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649

cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709

ttttaagggt taagggtgta ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769

taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata attgtagaca 2829

aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889

agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag tagaatttc 2948

<210> 65

<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp

1.

5

10

15

Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu

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Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly
20 25 30
35 40 45

Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala
50 55 60

Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly
65 70 75 80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp
85 90 95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys
100 105 110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu
115 120 125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met
130 135 140

Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys
145 150 155 160

Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu
165 170 175

Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr

180

185

190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg

195

200

205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His

210

215

220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val

225

230

235

240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile

245

250

255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp

260

265

270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn

275

280

285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys

290

295

300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile

305

310

315

320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly

325

330

335

209/735

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His

340

345

350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe

355

360

365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe

370

375

380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr

385

390

395

400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr

405

410

415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser

420

425

430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val

435

440

445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp

450

455

460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg

465

470

475

480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met

210/735

485

490

495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr

500

505

510

Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser

515

520

525

Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp

530

535

540

Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly

545

550

555

560

Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys

565

570

575

Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg

580

585

590

Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro

595

600

605

Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile

610

615

620

Ser Gly Ser Gly Tyr Gln Leu Val

625

630

<210> 66

<211> 4715

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (108).. (2003)

<400> 66

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cctccgcctc gcccagagccc cgggaggggtg aaacgctttc tcccagc atg cag cgg 116

Met Gln Arg

1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164

Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp

5

10

15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212

Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro

20

25

30

35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260

Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr

40

45

50

cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308
His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr

55

60

65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta 356
Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val

70

75

80

cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc 404
Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile

85

90

95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452
Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile

100

105

110

115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500
Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala

120

125

130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548
Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly

135

140

145

gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596
Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu

150

155

160

gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644

213/735

Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys

165

170

175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692

Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met

180

185

190

195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740

Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu

200

205

210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788

Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr

215

220

225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836

Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu

230

235

240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884

Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu

245

250

255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932

Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn

260

265

270

275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980

His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe

214/735

280	285	290	
ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta 1028			
Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu			
295	300	305	
gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta 1076			
Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu			
310	315	320	
aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg 1124			
Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp			
325	330	335	
gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat 1172			
Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His			
340	345	350	355
agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat 1220			
Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr			
360	365	370	
gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc 1268			
Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile			
375	380	385	
cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga 1316			
His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly			
390	395	400	
215/735			

aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa 1364
 Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln
 405 410 415

aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc 1412
 Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu
 420 425 430 435

agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa 1460
 Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys
 440 445 450

cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc 1508
 His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys
 455 460 465

cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg 1556
 Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met
 470 475 480

ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt 1604
 Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly
 485 490 495

tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat 1652
 Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp
 500 505 510 515

gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg 1700
 Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met

520 525 530

ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta 1748
 Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val

535 540 545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796
 Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr

550 555 560

aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca 1844
 Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr

565 570 575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata 1892
 Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile

580 585 590 595

gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg 1940
 Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val

600 605 610

gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct 1988
 Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser

615 620 625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg 2043

217/735

Gly Tyr Gln Leu Val

630

cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga 2103

gcatgctatg tgtagggcta atgggtgaatt ttacagtctt tttttcaaca cttttattaa 2163

caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

taattttaat ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct 2283

cacagtattt ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat 2343

cagaaatggt cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc 2403

agtctagtag gagtattgca tctaattcca ggagcattgt ttttaagttga ttgactagtt 2463

attatgtaca tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc 2523

tactgtgatg ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca 2583

atgttttggt tctatcagct gttgcaatgc tgatataatt ctagttcagt gaaataattt 2643

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tgtatactag cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa 2823

acagttccat ttttaagggt taagggtgta ttttcaagaa aaggcagaac aaataatgca 2883

aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata 2943

attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003

tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaatgacc tatcagaaag 3063

tagaatttca tcccaagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123

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atttggttta ttcattctaa gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303

ctgtgagagg gaatggggtg ggagatgtgg gggaatgggtg gtcagactga tgacagatcc 3363

tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423

gtgtctgtgt tagtgttttt aaagctgctc atttcatttt gtccaaccaa aaagaaaagg 3483

gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543

caagttcact gcatgtctga tgcttggtaa aactagtctt ccctgtaaaa tgcagattac 3603

aggtattaaa gcaatctagt ggtatacccg ccccttgctt tagtaagagg agcagtgaaa 3663

tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723

ataagtcaca catcaaaaaa agattaccct tagtgtatgt gttttaatat tagaaaattg 3783

gcatatgtac tttatTTTTg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattgggt aactttacaa atgtcagcta gttttgacta 3903

ctaattgggg gaaattttag ataattttta aattcaaagt tatttataaa atgctagaat 3963

ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg 4023

aatacatttt tatcaacagt taaagactat ggtggTTTT tcagagtttg gctaagaatg 4083

ttgttaccat cttctttgtt tgtgttacia tattttcagt gcaaaagaga tgctattcag 4143

ttaaaaagac aaacctctag atgtgtaatt acatggaaaa tactagcaat gtgaatgctt 4203

ttgtagtaac catctttag tacctgtgaa atctataact cagaaatggg cagatgggtca 4263

ggagccagct atgcagcagt ataccatctg ttttaattatt ttgtaggtcc tgtgtgtgga 4323

accaactata aaccagttc taaagtgtg tatgatggg aacctttggg aatagttctt 4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

tacttccttg gagttttttt tcattcatat tttgttgtt tccaggaatt tatttgatat 4503

taatgggcgt aaaacagcat cattgtactt aagctatgga tgtttttatt ttatatTTTc 4563

tttatttata actgtgccaa gtattatattt gctacttacc gtgttattct gtggaaagaa 4623

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taaaatatta atcagaataa atactgactc tt 4715

<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

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85

90

95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
100 105 110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
115 120 125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
130 135 140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145 150 155 160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
165 170 175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
180 185 190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
195 200 205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
210 215 220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225 230 235 240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
275 280 285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
290 295 300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305 310 315 320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
325 330 335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
355 360 365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385 390 395 400

223/735

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser

405

410

415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe

420

425

430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu

435

440

445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln

450

455

460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp

465

470

475

480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe

485

490

495

Ser Cys

<210> 68

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

224/735

<221> CDS

<222> (22).. (1515)

<400> 68

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gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51
                Met Ala Arg Leu Glu Val Ile Glu Leu Pro
                  1             5             10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
                15             20             25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
                30             35             40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
                45             50             55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
                60             65             70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
                75             80             85             90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
                225/735

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Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95 100 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387

Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg

110 115 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435

Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu

125 130 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483

His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly

140 145 150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531

Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn

155 160 165 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579

Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175 180 185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627

Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190 195 200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

226/735

205 210 215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
220 225 230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
235 240 245 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
255 260 265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
270 275 280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
285 290 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
300 305 310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
315 320 325 330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059

Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly

335

340

345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107

Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350

355

360

cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca 1155

His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser

365

370

375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203

Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly

380

385

390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251

Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp

395

400

405

410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299

Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415

420

425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347

Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile

430

435

440

tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta 1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu

445

450

455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala

460

465

470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser

475

480

485

490

cag aaa ctt tgg gaa ttc tct tgt tagttggta gttttactgt aattttctat 1545
Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttccttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat ttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85 90 95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala

100 105 110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met

115 120 125

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Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg

130

135

140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln

145

150

155

160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp

165

170

175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly

180

185

190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln

195

200

205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn

210

215

220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile

225

230

235

240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala

245

250

255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val

260

265

270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr

231/735

275 280 285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
290 295 300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305 310 315 320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
325 330 335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
355 360 365

Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385 390 395 400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu

435

440

445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln

450

455

460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp

465

470

475

480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe

485

490

495

Ser Cys

<210> 70

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22).. (1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51

Met Ala Arg Leu Glu Val Ile Glu Leu Pro

1

5

10

233/735

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
95 100 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
110 115 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435
 Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu

125

130

135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483
 His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly

140

145

150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531
 Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn

155

160

165

170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579
 Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175

180

185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627
 Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

195

200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675
 Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

205

210

215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723
 Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro

220

225

230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771

235/735

Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu

235 240 245 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819

Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala

255 260 265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867

Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys

270 275 280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915

Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp

285 290 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963

Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro

300 305 310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011

Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu

315 320 325 330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059

Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly

335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107

Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

236/735

350	355	360	
cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca 1155			
His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser			
365	370	375	
tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203			
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly			
380	385	390	
act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251			
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp			
395	400	405	410
ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299			
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg			
415	420	425	
tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347			
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile			
430	435	440	
tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta 1395			
Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu			
445	450	455	
cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443			
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala			
460	465	470	

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttggta gttttactgt aattttctat 1545
Gln Lys Leu Trp Glu Phe Ser Cys
495

aaagaattca tatcatctgt taatggcgac agtttttgtt tcttccttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcaggat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgacctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
238/735

1 5 10 15
Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
 20 25 30
Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
 35 40 45
Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
 50 55 60
Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
 65 70 75 80
Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
 85 90 95
Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp
 100 105 110
Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr
 115 120 125
Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
 130 135 140
Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
 145 150 155 160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
165 170 175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
180 185 190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
195 200 205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
210 215 220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
225 230 235 240

Gln Trp Ile Gln Arg
245

<210> 72

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127)..(861)

<400> 72

240/735

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ccaagccccg ccgatcgcgg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120

acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser

1

5

10

atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216

Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser

15

20

25

30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264

Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile

35

40

45

ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac 312

Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His

50

55

60

cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg 360

Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg

65

70

75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408

Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser

80

85

90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456

241/735

Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile

95 100 105 110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504

Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe

115 120 125

agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552

Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys

130 135 140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600

Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu

145 150 155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648

Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn

160 165 170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc 696

Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile

175 180 185 190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744

Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly

195 200 205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att 792

Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile

242/735

210 215 220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt 840
Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val

225 230 235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact 891
Leu Gly Gln Trp Ile Gln Arg

240 245

gtcagaaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

ctagggtctg tgaacgaggc ctgtctcttc cctgggggttt ctttccatgg cctttatttc 1011

tcctcttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggtg 1071

ggcctcggct tcgctggagt gtactccagg gtgaaggcag agtgggattt gagaccag 1131

tagtggagga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191

tcaccgggca tagcctggaa gcccgaagtc tgttctgact ttgcctggct gtctccttga 1251

cccgctcct agatcattgt ccttgatgtc caggctgggt catttaaaat agagatgcaa 1311

tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371

tcagcacctg agtcacagcc caggtgcccg gaagcagcct cttcgcatag gcagtgattt 1431

gcgattactt taaagctcac cttttttctt cccctctctg ttcgctgctg tcagcataat 1491

243/735

gattgtgttc cttccctatg ggatccatct gttttgtaaa caataaagcg tctgagggag 1551

<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

1

5

10

15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20

25

30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35

40

45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50

55

60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65

70

75

80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

85

90

95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

244/735

100	105	110	
Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu			
115	120	125	
Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro			
130	135	140	
Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His			
145	150	155	160
Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly			
165	170	175	
Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly			
180	185	190	
Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val			
195	200	205	
Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln			
210	215	220	
Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp			
225	230	235	240
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe			
245	250	255	

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
260 265 270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
275 280 285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
290 295 300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305 310 315 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
325 330 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
340 345 350

<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 74

246/735

ttaggcgggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc 60

tatccttggc gccacagtcg gccaccgggg ctgcccgcg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5 10 15 20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25 30 35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40 45 50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile

55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354

Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val

70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402

Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys

85 90 95 100

247/735

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
 Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
 105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498
 Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
 120 125 130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546
 Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
 135 140 145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594
 Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
 150 155 160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642
 Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
 165 170 175 180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690
 Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
 185 190 195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738
 Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
 200 205 210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786
 Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
 215 220 225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834
 Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
 230 235 240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882
 Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
 245 250 255 260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930
 Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
 265 270 275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978
 Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
 280 285 290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026
 Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
 295 300 305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074
 Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
 310 315 320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122
 249/735

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325 330 335 340

cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

345 350

gaagccgcac agcttgacct ggaagcacc cgtccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

togggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468

caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggatgaatcg 1528

ttgcttgctg tggacttggg ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708

tttccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctgcctcct gaaggacga gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgtttctcc ttgtgttacc cctcccagt attaccattt gccctcacc tgcccttggg 2188

gagcctttta gtgcaagaca gatggggctg tttcccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcac tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

1

5

10

15

251/735

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20

25

30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35

40

45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50

55

60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65

70

75

80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

85

90

95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

100

105

110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu

115

120

125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro

130

135

140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His

145

150

155

160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly

252/735

165 170 175
Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
180 185 190
Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
195 200 205
Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
210 215 220
Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225 230 235 240
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
245 250 255
Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
260 265 270
Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
275 280 285
Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
290 295 300
Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305 310 315 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
 325 330 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
 340 345 350

<210> 76
 <211> 2401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (103)..(1158)

<400> 76
 ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc 60

tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga 114
 Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162
 Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
 5 10 15 20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210
 Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
 254/735

25	30	35	
caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258			
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys			
40	45	50	
agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306			
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile			
55	60	65	
gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354			
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val			
70	75	80	
gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402			
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys			
85	90	95	100
atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450			
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile			
105	110	115	
att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498			
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu			
120	125	130	
gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546			
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val			
135	140	145	

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
150 155 160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
165 170 175 180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
185 190 195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
200 205 210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
215 220 225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
230 235 240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
245 250 255 260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930

Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln

265

270

275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978

Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro

280

285

290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026

Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser

295

300

305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074

Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310

315

320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325

330

335

340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

345

350

gaagccgcac agcttgacct ggaagcacc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actotccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

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caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggatgaatcg 1528

ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccaggtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgcaggctg ggcaggtcaa cttgtgttcc 1708

tttccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgccagat ggtcggggcc ccgggcaaca gattgaagag 1828

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gaactcctgc cacttgggag agctcgggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

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tcgtttctcc ttgtgttacc cctcccagt attaccattt gccctcacc tgcccttggt 2188

gagcctttta gtgcaagaca gatggggctg ttttcccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcac tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc 2401

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<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala

1 5 10 15

Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser

20 25 30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile

35 40 45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile

50 55 60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile

65 70 75 80

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Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn

85

90

95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser

100

105

110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu

115

120

125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser

130

135

140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu

145

150

155

160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys

165

170

175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile

180

185

190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe

195

200

205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile

210

215

220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp

260/735

225 230 235 240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu
 245 250 255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met
 260 265 270

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr
 275 280 285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe
 290 295 300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His
305 310 315 320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp
 325 330 335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe
 340 345 350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala
 355 360 365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser
 370 375 380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe

385 390 395 400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile

405 410 415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu

420 425 430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu

435 440 445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly

450 455 460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys

465 470 475 480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp

485 490 495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp

500 505 510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp

515 520 525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu

530 535 540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn

545 550 555 560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp

565 570 575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp

580 585 590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys

595 600 605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp

610 615 620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met

625 630 635 640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp

645 650 655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys

660 665 670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr

675 680 685

Gly Gln Gly Phe Lys Leu Val Lys Ser

263/735

690

695

<210> 78

<211> 3008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (372)..(2462)

<400> 78

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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttcccca 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aatttttgta acgtgagga aaagcccaca 360

ttgctggtta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu

1

5

10

tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458

Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met

15

20

25

cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg 506

His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu

30

35

40

45

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554

Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn

50

55

60

tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602

Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile

65

70

75

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650

Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser

80

85

90

ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt 698

Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu

95

100

105

gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746

Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr

110

115

120

125

ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag 794

265/735

Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu
130 135 140

aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt 842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val
145 150 155

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg 890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu
160 165 170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg 938
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met
175 180 185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta 986
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu
190 195 200 205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa 1034
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys
210 215 220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct 1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro
225 230 235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa 1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys
266/735

240	245	250	
ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt			1178
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe			
255	260	265	
gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt			1226
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu			
270	275	280	285
aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt			1274
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe			
290	295	300	
gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg			1322
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp			
305	310	315	
gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac			1370
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His			
320	325	330	
agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg			1418
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met			
335	340	345	
cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt			1466
Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu			
350	355	360	365

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att 1514

Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile

370

375

380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat 1562

Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His

385

390

395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga 1610

Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly

400

405

410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca 1658

Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro

415

420

425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act 1706

Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr

430

435

440

445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag 1754

Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu

450

455

460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg 1802

Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu

465

470

475

cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc 1850

His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro

480

485

490

aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca 1898

Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr

495

500

505

gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt 1946

Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu

510

515

520

525

ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att 1994

Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile

530

535

540

atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg 2042

Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg

545

550

555

aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa 2090

Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys

560

565

570

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138

Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr

575

580

585

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186

Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
 590 595 600 605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234
 Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
 610 615 620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282
 Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
 625 630 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330
 His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
 640 645 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378
 Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
 655 660 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426
 Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
 670 675 680 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttgac 2472
 Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
 690 695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532

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tggccaatga tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat 2832

gtagaccaga taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt 2892

ctttttcca aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct 2952

tagaaaagaa agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3008

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<211> 611

<212> PRT

<213> Homo sapiens

<400> 79

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Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val

20 25 30

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg

35

40

45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg

50

55

60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala

65

70

75

80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu

85

90

95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser

100

105

110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe

115

120

125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe

130

135

140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu

145

150

155

160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys

165

170

175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe

180

185

190

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Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val

195

200

205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile

210

215

220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys

225

230

235

240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg

245

250

255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln

260

265

270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser

275

280

285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu

290

295

300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys

305

310

315

320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe

325

330

335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln

273/735

340 345 350
Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe
355 360 365
Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser
370 375 380
Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu
385 390 395 400
Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr
405 410 415
Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp
420 425 430
Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly
435 440 445
Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr
450 455 460
Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val
465 470 475 480
Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro
485 490 495

Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn

500

505

510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala

515

520

525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro

530

535

540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile

545

550

555

560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu

565

570

575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met

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595

600

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Val Lys Ser

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<213> Homo sapiens

275/735

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<221> CDS

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ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcactgcgtt attgctttag tcattgtctc tatntagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggtatcttg 480

ctatttagcc agaatcaatt tattggttgc tatatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652

Met Glu Ala Ala Ser Leu Ser Leu

1

5

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tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700
 Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp
 10 15 20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748
 Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu
 25 30 35 40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796
 Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg
 45 50 55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844
 Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu
 60 65 70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892
 Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val
 75 80 85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940
 Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu
 90 95 100

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt 988
 Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val
 105 110 115 120

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat 1036

Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn

125

130

135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc 1084

Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe

140

145

150

ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc 1132

Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro

155

160

165

ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct 1180

Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala

170

175

180

gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga 1228

Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg

185

190

195

200

gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga 1276

Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly

205

210

215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga 1324

Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly

220

225

230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg 1372

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Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg
 235 240 245

aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc 1420
 Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg
 250 255 260

cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca 1468
 His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala
 265 270 275 280

aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc 1516
 Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe
 285 290 295

ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg 1564
 Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly
 300 305 310

ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat 1612
 Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr
 315 320 325

gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca 1660
 Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr
 330 335 340

ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc 1708
 Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly
 279/735

345 350 355 360
atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc 1756
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr
365 370 375
tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat 1804
Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His
380 385 390
tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga 1852
Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg
395 400 405
cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga 1900
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly
410 415 420
gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata 1948
Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile
425 430 435 440
gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc 1996
Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile
445 450 455
gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa 2044
Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys
460 465 470
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att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca 2092

Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr

475

480

485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa 2140

Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys

490

495

500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act 2188

Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr

505

510

515

520

gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg 2236

Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp

525

530

535

agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac 2284

Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His

540

545

550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca 2332

Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala

555

560

565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380

Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe

570

575

580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428

Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu

585

590

595

600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481

Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

605

610

gatattaata agcactcata ctaccaatta tcactaactt gccatTTTT gtatgctgta 2541

tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcacttg tcttttctta 2601

agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa gtatgtaggg 2661

agtcaaagtc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721

tgtttgctta tggctctgat tagaaagaaa cagttgtcta tgctctgcaa tggatcaatga 2781

tgaattacta atgccttatt ttctaggcat ataataatag ttagagaat gtagaccaga 2841

taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca 2901

aacagtaggt ttcacccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa 2961

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3007

<210> 81

<211> 184

<212> PRT

<213> Homo sapiens .

<400> 81

Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu

1 5 10 15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln

20 25 30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys

35 40 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln

50 55 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser

65 70 75 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu

85 90 95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro

100 105 110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys

115 120 125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser

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130 135 140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile

145 150 155 160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro

165 170 175

Thr Glu Met Asp Glu Asn Glu Ser

180

<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (285)..(836)

<400> 82

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gcgcgcgcgg gagcgcggga ggatcggcgg ctgcgggtca ctggtccctg gctcggttcc 120

ccgcaccccg gggtcacac ttaccgcgcg ggaggagcag cggccgggtg tccaccccca 180

tcctgcgcc agtctcctcg attcccctcg ctctgagccg ggagagccga acagctgaag 240

agagttcact gactccccag cccaggtgg gccttggtgca catc atg acc agt ttt 296

Met Thr Ser Phe

1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val

5

10

15

20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392

Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe

25

30

35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440

Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn

40

45

50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488

Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val

55

60

65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser

70

75

80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc 584

Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser

85

90

95

100

aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg 632

Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met

105

110

115

gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag 680

Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu

120

125

130

tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc 728

Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu

135

140

145

ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc 776

Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly

150

155

160

act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat 824

Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp

165

170

175

180

gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa 876

Glu Asn Glu Ser

gagctctgta gatgctgtat agacactaaa taagagttga ttagggtagt atattatagt 936

catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996

ttagtcatta acttagtcac ctgttgatt ctggatctac acaaaattat tttaactgct 1056

cttattaatc tgtgaggatt aatatacaaa aagtatcctt tgagatgaag tcgtgttctc 1116

aaaataaggt tatattatct tctttttctg ctgattttc atcttgtgtt ttgctttgtt 1176

tttgtaagga accatctctt ggtttggtca catcagttca caacagccat ttgttttcaa 1236

ggtcaaggct ccaggcaggt tgttactggt gtttgagcc tgcagtact tgcagtactg 1296

gaatagggtc taggctagtg tctgcgcgtc actgtgggtt tagcatggga ggacttattt 1356

gagaaatact accttacttt tctatgattt ctttttacag agttatagtg tgtttactcc 1416

taagatgaca gttctctttg tctatattca gcatctaaga caaatattta aacattttta 1476

agaaccactg tgtaagttt aggattattt acttaccaaa ttagaagttt gacttttatg 1536

tggtatacac aatcttaaaa ttccacgaat tcacctttt aatagtatcc atgtacataa 1596

taaaatcaaa gtttaattag c 1617

<210> 83

<211> 392

<212> PRT

<213> Homo sapiens

<400> 83

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

10

15

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Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20

25

30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35

40

45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50

55

60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65

70

75

80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85

90

95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

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165	170	175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser		
180	185	190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser		
195	200	205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met		
210	215	220
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr		
225	230	235
240		
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser		
245	250	255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu		
260	265	270
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr		
275	280	285
Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu		
290	295	300
Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly		
305	310	315
320		

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
325 330 335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
340 345 350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
355 360 365

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
370 375 380

Val Glu Ser Pro Val Gln Lys Val
385 390

<210> 84

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1294)

<400> 84

acttccgctg gccgctggct cgctggccgc tcctggaggc ggcggcggga gcgcaggggg 60

cgcgcgggccc ggggactcgc attccccggt tccccctcca cccacgcgg cctggacc 118
290/735

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35 40 45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50 55 60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100 105 110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838
292/735

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 982
 Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
 275 280 285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc 1030
 Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
 290 295 300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078
 Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
 305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126
 Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
 325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174
 Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
 293/735

340 345 350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222
Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

355 360 365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270
Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370 375 380

gtt gag tct cct gtg cag aag gtt tgaggggtgga aagggcctga ggggtgaagt 1324
Val Glu Ser Pro Val Gln Lys Val

385 390

gaaataggac cctccaccca tccccttctg ctgtaacctc tgaggagct ggctgaaagg 1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agttttattct 1504

gagccccggg ggtagacagt cctcagttag gggttttggg gagtttgggg tcaagagagc 1564

ataggtaggt tccacagtta ctcttccac aagttccctt aagtcttgcc ctagctgtgc 1624

tctgccacct tccagactca ctcccctctg caaatacctg catttcttac cctggtgaga 1684

aaagcacaag cgggtgtaggc tccaatgctg ctttcccagg aggggtgaaga tgggtgctgtg 1744

ctgaggaaag gggatgcaga gccctgccca gcaccaccac ctcctatgct cctggatccc 1804

294/735

taggctctgt tccatgagcc tgttgcaggt tttgtactt tagaaatgta actttttgct 1864

cttataattt tattttatta aattaaatta ctgc 1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
85 90 95

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Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

296/735

245 250 255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
260 265 270
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
275 280 285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
290 295 300
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305 310 315 320
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
325 330 335
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
340 345 350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
355 360 365
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
370 375 380
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385 390 395 400

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
405 410 415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
420 425 430

<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1414)

<400> 86

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cgcgcgggccc ggggactcgc attccccggt tccccctcca cccacgcgg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35

40

45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50

55

60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65

70

75

80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85

90

95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598

299/735

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 300/735

260	265	270	
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg			982
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp			
275	280	285	
cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt			1030
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe			
290	295	300	
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa			1078
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu			
305	310	315	320
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag			1126
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu			
325	330	335	
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag			1174
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln			
340	345	350	
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc			1222
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr			
355	360	365	
atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt			1270
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu			
370	375	380	
301/735			

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385 390 395 400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366
Val Phe Ala Ala Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
405 410 415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt 1414
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
420 425 430

tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg 1474

ctgtaacctc tgagggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca 1534

gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgcottaag 1594

tcacccatct tccagtaagc agtttattct gagccccggg ggtagacagt ctcagtgag 1654

gggttttggg gagtttggg tcaagagagc ataggtaggt tccacagtta ctcttccac 1714

aagttccctt aagtcttgcc ctagctgtgc tctgccacct tccagactca ctcccctctg 1774

caaataacctg catttcttac cctggtgaga aaagcacaag cgggtgtaggc tccaatgctg 1834

ctttcccagg aggggtgaaga tggtgctgtg ctgaggaaag gggatgcaga gccctgcca 1894

gcaccaccac ctcctatgct cctggatccc taggctctgt tccatgagcc tgttgaggt 1954

tttggacttt tagaaatgta actttttgct cttataattt tattttatta aattaaatta 2014

ctgc 2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser
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Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser
20 25 30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His
35 40 45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser
50 55 60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys
65 70 75 80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val
303/735

85	90	95
Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe		
100	105	110
Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala		
115	120	125
Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu		
130	135	140
Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser		
145	150	155
		160
Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu		
165	170	175
Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile		
180	185	190
Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg		
195	200	205
Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu		
210	215	220
Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala		
225	230	235

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (111).. (815)

<400> 88

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aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt 116

Met Gly

1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164

Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly

5

10

15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212

Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser

20

25

30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat 260

Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn

35

40

45

50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa 308
 Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu

55

60

65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg 356
 Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val

70

75

80

ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat 404
 Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn

85

90

95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag 452
 Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu

100

105

110

atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat 500
 Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn

115

120

125

130

ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat 548
 Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp

135

140

145

act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac 596
 Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn

150

155

160

agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat 644

306/735

Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn

165

170

175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc 692

Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala

180

185

190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt 740

Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe

195

200

205

210

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga 788

Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg

215

220

225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat 835

Asn Met Val Gln Arg Gln Phe Ile Ala

230

235

gtggctggct cttgttttgt aaaccaaagc attaatcttc acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955

taaatttctg caggacagcc tataaaattg tgggtactttt tgatgtttca gtaaacttga 1015

cattgtcaga gtttcaagga cttttctttc acaattttcc tagttcatgg atatgaaaaa 1075

ggaattctca atccatattc cttgtattga accttgaaca aaaacttgta tgacagacat 1135

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aatggcccc aggagatctg atcacacttc ctctgaggc acctctcatg gatgttgcaa 1255

taagcattcg ggtactatca ccagaaata tgaattgcca gaatagaaca tttagcatgt 1315

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cttctaaaag gcgtataact gtgtgagtgg ccagatattc actttttaga tcaaaaacct 1615

ctcttatgga agctttaaaa gtttccgtca cacacaattc tcttctcagg aagtatttct 1675

catttaggtc ttcaaagtag cctgactgtg tgcatgtgtg tgtgtgatag gttatttata 1735

aagactttgg atagaaggag atgtatttta ttacctcta ttctagagcc catgctcct 1795

aacaagccag agaggcccca aacaggattg tttctttcct ccacagccct tctgccatc 1855

tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggcatgtc 1915

atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcca 1975

ctgaggatga atgtaactgt gggcaacta tttaccctcc tttatctgtg aaatgaaagg 2035

gttgaattga tggatctcta aaggcttttg tcctctatga ggatgtgaaa aactagggac 2095

cacaaaaggg aacaagcaaa aaagtttgga ttcgataaag tgatatgtaa tagttgcaga 2155

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tttaatgctg tcattacact taaagtcaca ggaaaaaaat atacatgctt actcaggctt 2275

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tcttattccc cacttgata tcccctacca gtaccgggat ctgcacacat ctttttgag 2395

ttacctcttc atagccatga accaaaacgt tctatgagga gcatgcaagt aagtcaagcc 2455

tcctattctg ttagtactta ttagaggagg agatggtttt cattgcatag tgacattttc 2515

ttagccttaa cgttctgata gtagcttact actcacttct ctttttcagt tttcataata 2575

agtattcatt tttttgccat aatgcttcct gtaaagccaa ttttatatac taataaaaca 2635

tgaactgccc actcttcatg cctgccaaac ttggggcaat tgatgctaaa tggatattttt 2695

aaaataaatg tttttattct tt 2717

<210> 89

<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20 25 30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35 40 45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50 55 60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65 70 75 80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85 90 95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100 105 110

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115 120 125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130 135 140

310/735

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

145 150 155 160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

165 170 175

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val

180 185 190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu

195 200 205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

210 215 220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn

225 230 235 240

Gln Tyr Glu Ile Val

245

<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

<220>

311/735

<221> CDS

<222> (60).. (794)

<400> 90

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atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt 107

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

1 5 10 15

ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20 25 30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35 40 45

tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50 55 60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65 70 75 80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85 90 95

312/735

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395
 Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
 100 105 110

gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag 443
 Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
 115 120 125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta 491
 Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
 130 135 140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539
 Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
 145 150 155 160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt 587
 Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
 165 170 175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta 635
 Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
 180 185 190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa 683
 Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
 195 200 205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg 731

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

210

215

220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac 779

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn

225

230

235

240

cag tat gag ata gtg taacccaatg tatctgtggg cctattcttc tctaccttta 834

Gln Tyr Glu Ile Val

245

aggacattta gggccccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac 894

tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga 954

cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca 1014

atcaagatgt atgtttgcta tgttctaagt ccaccttcta tcccattcat gttagatcgt 1074

tgaaaccctg tatccctctg aaacactgga agagctagta aattgtaaata gaagtaatac 1134

tgtgttcctc ttgactgtta tttttcttag tagggggcct ttggaaggca ctgtgaattt 1194

gctatittga ttagtggtta caagatggaa aattgattcc tctgactttg ctattgatgt 1254

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gattgtataa tttgcaccaa gaagttaaaa tgttttatga ctctctgttc tgctgacagg 1374

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<210> 91

<211> 180

<212> PRT

<213> Homo sapiens

<400> 91

Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

1 5 10 15

Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu

20 25 30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala

315/735

35 40 45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

50 55 60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

65 70 75 80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

85 90 95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

100 105 110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

115 120 125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

130 135 140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

145 150 155 160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser

165 170 175

Ala Leu Leu Gln

180

<210> 92

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(565)

<400> 92

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Met Ala Ser Thr Ser Tyr Asp Tyr Cys

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Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly

10

15

20

25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148

Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu

30

35

40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196

Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu

45

50

55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244

Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu

317/735

60	65	70	
ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc			292
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala			
75	80	85	
acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag			340
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu			
90	95	100	105
aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act			388
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr			
110	115	120	
aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg			436
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu			
125	130	135	
aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac			484
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr			
140	145	150	
tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg			532
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu			
155	160	165	
att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc			585
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln			
170	175	180	
318/735			

acatcttgga aggtccgtcc tgctcggctt ttgcttgaa cattcccttg atctcatcag 645
ttctgagcgg gtcattggggc aacacggta gcggggagag cacgggtag ccggagaagg 705
gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765
ttgaccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc 825
tcccacctg agattgggca tggggtgcgg tgtggggggc atgtgctgcc tgttgttatg 885
ggtttttttt gcgggggggg ttgctttttt ctggggtctt tgagctcaa aaaataaaca 945
cttcctttga gggagagcac acctt 970

<210> 93

<211> 331

<212> PRT

<213> Homo sapiens

<400> 93

Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe

1

5

10

15

Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn

20

25

30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu

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35 40 45
Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala
50 55 60
Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp
65 70 75 80
Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile
85 90 95
Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly
100 105 110
Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly
115 120 125
Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr
130 135 140
Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala
145 150 155 160
Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser
165 170 175
Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu
180 185 190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser

195

200

205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile

210

215

220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr

225

230

235

240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala

245

250

255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr

260

265

270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu

275

280

285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu

290

295

300

Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln

305

310

315

320

Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His

325

330

<210> 94

321/735

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(1167)

<400> 94

attatgcaga tgcacggctg gaggtgggat ccacacagct cagaacagct ggatcttgct 60

cacactcttt caagagaagc ttccttgggt taagaaaaaa aacgaaccct tccagtcagg 120

tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg 177

Met

1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225

Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg

5

10

15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273

Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu

20

25

30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321

Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala

35

40

45

gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369

Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile

50

55

60

65

gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt 417

Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe

70

75

80

ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa 465

Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu

85

90

95

aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc 513

Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys

100

105

110

acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc 561

Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile

115

120

125

atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt 609

Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser

130

135

140

145

ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg 657

Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val

150

155

160

act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca 705

323/735

Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala

165

170

175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag 753

Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys

180

185

190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt 801

Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu

195

200

205

ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt 849

Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg

210

215

220

225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg 897

Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp

230

235

240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc 945

Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly

245

250

255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act 993

Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr

260

265

270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca 1041

Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser

324/735

275 280 285

aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg 1089
Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg

290 295 300 305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc 1137
Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile

310 315 320

tat cag cgt ctg aat cca tgc cat acc cac tgacccaga ccagtgcagc 1187
Tyr Gln Arg Leu Asn Pro Cys His Thr His

325 330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgttagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427

atttccttta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547

ttttggatac agcagaagaa acagcggtc cactaccgac ctgccccgg ttcgatgtcc 1607

ttccaagaat gaagtctttc cctggtgatg gtcccctgcc ctgtctttcc agcatccact 1667

325/735

ctgtcttgtc ctcttggaag tgtatctcag tcagccagtg gcttcttgat gatggcggtg 1727

gaggtgggtg ttgtagtgtg atggatcccc tttaggttat ttaggggtat atgtcccctg 1787

cttgaaccct gaaggccagg taatgagcca tggccattgt cccagctga ggaccaggtg 1847

tctctaaaaa cccaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907

ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967

gggaggccgg atctctagag ccatacctgct gaggccctg tgtgtaagtc ctaataaact 2027

cacctactca cc 2039

<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1 5 10 15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20 25 30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

326/735

35 40 45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
50 55 60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
65 70 75 80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
85 90 95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
100 105 110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
115 120 125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
130 135 140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145 150 155 160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
165 170 175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
180 185 190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
195 200 205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
210 215 220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225 230 235 240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
245 250 255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
260 265 270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
275 280 285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
290 295 300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305 310 315 320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
325 330 335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
340 345 350
328/735

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser

355

360

365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu

370

375

380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe

385

390

395

400

Val Cys Lys Tyr Lys Leu Leu

405

<210> 96

<211> 1409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (181)..(1401)

<400> 96

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ttcccactag ccggagtagc ctctagtctg ttagtcaaaa cgtgaaaaaa aaagacctgc 120

tttgccctgg gaaatagtaa ccctgcaaaa tacatcagct tgtaggagac agaggatgtg 180

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atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1

5

10

15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20

25

30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35

40

45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

50

55

60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65

70

75

80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85

90

95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100

105

110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc 564

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115

120

125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc 612

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130

135

140

ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc 660

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

145

150

155

160

ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act 708

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

165

170

175

aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca 756

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

180

185

190

ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa 804

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys

195

200

205

ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc 852

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr

210

215

220

atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa 900

331/735

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys

225 230 235 240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga 948

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg

245 250 255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg 996

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu

260 265 270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac 1044

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp

275 280 285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc 1092

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly

290 295 300

aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta 1140

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu

305 310 315 320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta 1188

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu

325 330 335

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser

332/735

340	345	350	
aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca			1284
Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser			
355	360	365	
gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa			1332
Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu			
370	375	380	
aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt			1380
Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe			
385	390	395	400
gtg tgc aaa tat aaa cta tta taaaatcg			1409
Val Cys Lys Tyr Lys Leu Leu			
405			

<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

1

5

10

15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

333/735

20 25 30
His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
35 40 45
Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
50 55 60
Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
65 70 75 80
Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
85 90 95
Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
100 105 110
Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
115 120 125
Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val
130 135 140
Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145 150 155 160
Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
165 170 175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu

180

185

190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr

195

200

205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

210

215

220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser

225

230

235

240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp

245

250

255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr

260

265

270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg

275

280

285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290

295

300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln

305

310

315

320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val

325

330

335

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Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp

340

345

350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val

355

360

365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr

370

375

380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro

385

390

395

400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu

405

410

415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys

420

425

430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro

435

440

445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly

450

455

460

Asp

465

<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477).. (1871)

<400> 98

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ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagaggggcc 180
tggtgtatca ctggaggaaa tagcctgccca aggaatacac gtcttcagaa gaagttctgt 240
gtggcttcaa gagactgata aaattgtgag aggaaaacag cctaccgggt cctcttttct 300
tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360
ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420
tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

337/735

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser	
5 10 15	
atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac	575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His	
20 25 30	
agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa	623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln	
35 40 45	
aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca	671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro	
50 55 60 65	
ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att	719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile	
70 75 80	
gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga	767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly	
85 90 95	
gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg	815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp	
100 105 110	
cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt	863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val	
338/735	

115 120 125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca 911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr
130 135 140 145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
150 155 160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
165 170 175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
180 185 190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
195 200 205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210 215 220 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
230 235 240

339/735

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247

Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala

245

250

255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295

Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

260

265

270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343

Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

275

280

285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391

His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

290

295

300

305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439

Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu

310

315

320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487

Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325

330

335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535

Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

340

345

350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583

Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln

355

360

365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631

Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu

370

375

380

385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679

Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr

390

395

400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727

Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp

405

410

415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

450

455

460

465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag

1940

<210> 99

<211> 465

<212> PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

1

5

10

15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

20

25

30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser

35

40

45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala

50

55

60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu

65

70

75

80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His

85

90

95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys

342/735

100	105	110
Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu		
115	120	125
Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val		
130	135	140
Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser		
145	150	155
160		
Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg		
165	170	175
Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu		
180	185	190
Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr		
195	200	205
Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn		
210	215	220
Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser		
225	230	235
240		
Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp		
245	250	255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr

260

265

270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg

275

280

285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290

295

300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln

305

310

315

320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val

325

330

335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp

340

345

350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val

355

360

365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr

370

375

380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro

385

390

395

400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu

405

410

415

344/735

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys

420

425

430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro

435

440

445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly

450

455

460

Asp

465

<210> 100

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477).. (1871)

<400> 100

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caccaaattc cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

345/735

tggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgac aaattgtgag aggaaaacag cctaccgggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgagggtga ttttcatcac ggtggaaaat 420

tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

20

25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35

40

45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

50

55

60

65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

70

75

80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

85

90

95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

100

105

110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca 911

Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr

130

135

140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

150

155

160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007

Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

165

170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055

347/735

Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
 180 185 190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103
 Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
 195 200 205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151
 Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
 210 215 220 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199
 Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
 230 235 240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247
 Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
 245 250 255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295
 Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
 260 265 270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343
 Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
 275 280 285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391
 His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
 348/735

290	295	300	305	
att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag				1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu				
	310	315	320	
aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg				1487
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu				
	325	330	335	
ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt				1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val				
	340	345	350	
ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag				1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln				
	355	360	365	
agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc				1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu				
370	375	380	385	
agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act				1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr				
	390	395	400	
tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac				1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp				
	405	410	415	
				349/735

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

450

455

460

465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataatccca 1931

taagggcag

1940

<210> 101

<211> 685

<212> PRT

<213> Homo sapiens

<400> 101

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys

1

5

10

15

Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys

20

25

30

350/735

Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln

35

40

45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His

50

55

60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys

65

70

75

80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys

85

90

95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile

100

105

110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp

115

120

125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln

130

135

140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu

145

150

155

160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val

165

170

175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly

351/735

180 185 190
Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
195 200 205
Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
210 215 220
Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
225 230 235 240
Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
245 250 255
His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
260 265 270
Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
275 280 285
Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
290 295 300
Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
305 310 315 320
Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
325 330 335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
340 345 350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
355 360 365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
370 375 380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
385 390 395 400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
405 410 415

Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr
420 425 430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
435 440 445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
450 455 460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465 470 475 480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
485 490 495

353/735

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn

500

505

510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu

515

520

525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val

530

535

540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp

545

550

555

560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser

565

570

575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val

580

585

590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser

595

600

605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn

610

615

620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu

625

630

635

640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg

354/735

645 650 655
Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
660 665 670
Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
675 680 685

<210> 102

<211> 2783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (128)..(2182)

<400> 102

gcacaagtgg accggggtgt tgggtgctag tcggcaccag aggcaagggt gcgaggacca 60

cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtgc ggggcggcaa 120

ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser

1

5

10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217

Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser

355/735

15	20	25	30	
aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag				265
Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln				
	35	40	45	
tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat				313
Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His				
	50	55	60	
tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act				361
Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr				
	65	70	75	
ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca				409
Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala				
	80	85	90	
aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca				457
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala				
	95	100	105	110
aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag				505
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys				
	115	120	125	
att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta				553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val				
	130	135	140	
				356/735

gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc 601

Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu

145

150

155

ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga 649

Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg

160

165

170

aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg 697

Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val

175

180

185

190

tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc 745

Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu

195

200

205

aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg 793

Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly

210

215

220

gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga 841

Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg

225

230

235

acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa 889

Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys

240

245

250

caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg 937
Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met
255 260 265 270

tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa 985
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys
275 280 285

gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca 1033
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser
290 295 300

ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac 1081
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn
305 310 315

cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt 1129
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe
320 325 330

ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca 1177
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr
335 340 345 350

gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa 1225
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys
355 360 365

gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att 1273
358/735

Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile
370 375 380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt 1321
Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu
385 390 395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac 1369
Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His
400 405 410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct 1417
Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser
415 420 425 430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg 1465
Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg
435 440 445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc 1513
Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys
450 455 460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt 1561
Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val
465 470 475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa 1609
Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys
359/735

480	485	490	
gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac			1657
Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr			
495	500	505	510
tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt			1705
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly			
	515	520	525
gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa			1753
Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys			
	530	535	540
aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca			1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala			
	545	550	555
aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac			1849
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr			
	560	565	570
ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct			1897
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro			
575	580	585	590
agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta			1945
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu			
	595	600	605
360/735			

aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag 1993

Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln

610

615

620

gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat 2041

Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn

625

630

635

gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act 2089

Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr

640

645

650

ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa 2137

Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys

655

660

665

670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac 2182

Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn

675

680

685

tgaaagactt ttcgaatgga ccctatggga ctctctttt ccactgtgag atctacaggg 2242

aacccaaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302

attcccctgt ggcctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362

actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422

ggtttttcag acaattttgc agaaagggtgc attgattctt aaattctctc tgttgagagc 2482

atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaaggag 2542

gaagctccca tgttgtttaa aggctgtaat tggagcagct tttggctgcg taactgtgaa 2602

ctatggccat atataatttt ttttcattaa tttttgaaga tacttgtggc tggaaaagtg 2662

cattccttgt taataaacit tttattttatt acagcccaaa gagcagtatt tattatcaaa 2722

atgtcttttt ttttatgttg accattttta accgttggca ataaagagta tgaaaacgca 2782

g 2783

<210> 103

<211> 161

<212> PRT

<213> Homo sapiens

<400> 103

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala

1 5 10 15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr

20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35 40 45

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Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln

50

55

60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr

65

70

75

80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys

85

90

95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly

100

105

110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile

115

120

125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val

130

135

140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg

145

150

155

160

Leu

<210> 104

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (552)

<400> 104

ccttttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15

20

25

30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35

40

45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50

55

60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

65

70

75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met

80

85

90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn

95

100

105

110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly

115

120

125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln

130

135

140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145

150

155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctgggtgga gggtctgccc tgggtgtctc 652

acctctccag ggggccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

365/735

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgccaga gctcggctga accagccttt agtcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggtt 1072

tgagattctg taactgcaga ctccattagc acacagattc actttaattt cttaattttt 1132

tttttaata caaggagggg gctattaaca ccagtagag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgcc tgtctccct tgtttctctg 1252

tgccagatct tcagtgcctt tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaca gagatggggt ctactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

<210> 105

<211> 161

<212> PRT

<213> Homo sapiens

<400> 105

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
1 5 10 15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
367/735

115

120

125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val

130

135

140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg

145

150

155

160

Leu

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (552)

<400> 106

ccttttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

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Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15 20 25 30
 agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207
 Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
 35 40 45
 ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255
 Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
 50 55 60
 acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303
 Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
 65 70 75
 gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351
 Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met
 80 85 90
 tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
 Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95 100 105 110
 gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
 Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
 115 120 125
 tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
 Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
 369/735

130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctgggtgga ggttctgccc tgggtggtctc 652

acctctccag ggggccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggtt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaatttt 1132

tttttaaata caaggagggg gctattaaca ccagtacag acatatccac aaggtcgtaa 1192

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atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcgcc tttccataca gggatTTTTT tctcatagag taattatatg 1312

aacagTTTTT atgacctcct ttgggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaa gagatgggggt cttactatgt tgcccaggct ggtgtcgaaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val

1 5 10 15

Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val

20 25 30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys

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35 40 45

Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn
50 55 60

Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu
65 70 75 80

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met
85 90 95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val
100 105 110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys
115 120 125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro
130 135 140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro
145 150 155 160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met
165 170 175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu
180 185 190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His

195

200

205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val

210

215

220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile

225

230

235

240

Gly Phe Phe Leu Gly Lys Phe Ile Leu

245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232).. (978)

<400> 108

agtgcgcgtg gccgtggcgg ctggtgtggg gttgagtcag ttgtgggacc cggagctgct 60

gaccagcgg gtggcccacc gaaccggtga cacagcggca ggcgttaggg ctcgggagcc 120

gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgcccc 180

agtcagcaaa ccgccgccgc gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg 237

Met Ala

1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285

Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

5

10

15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333

Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr

20

25

30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381

Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys

35

40

45

50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429

Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly

55

60

65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477

Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro

70

75

80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

85

90

95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573

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Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys

100 105 110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621

Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe

115 120 125 130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669

Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys

135 140 145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717

Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro

150 155 160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765

His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu

165 170 175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg 813

Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg

180 185 190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861

His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp

195 200 205 210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909

Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser

375/735

215 220 225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957
Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe

230 235 240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttcct 1008
Phe Leu Gly Lys Phe Ile Leu

245

ttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcac ttgtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacgggta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtcc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

tgttatttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368

atttagattg ctaatccac tcattcagga aatgccaaga ggtattcctt ggggaaatgg 1428

tgccctttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcac cttacaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaaat aaaactgtta acagattcctt gctcgat 1595

376/735

<210> 109

<211> 540

<212> PRT

<213> Homo sapiens

<400> 109

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

1 5 10 15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20 25 30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

100 105 110

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Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270
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Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln

275

280

285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro

290

295

300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser

305

310

315

320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu

325

330

335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly

340

345

350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys

355

360

365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys

370

375

380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala

385

390

395

400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg

405

410

415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu

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420

425

430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435

440

445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

450

455

460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465

470

475

480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485

490

495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500

505

510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

515

520

525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

530

535

540

<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102).. (1721)

<400> 110

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gaggaccac ctctgagtgt ccagtgtca gttgcccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

1

5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

60

65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

381/735

70	75	80	85	
ctc	caa	cag	gaa	aag
ctg	cta	cct	gcc	caa
ctc	cct	gct	gaa	aag
gaa				404
Leu	Gln	Gln	Glu	Lys
Leu	Leu	Pro	Ala	Gln
Leu	Pro	Ala	Glu	Lys
Glu				
	90	95	100	
gtg	ggt	ccc	cct	ctc
cct	cag	gaa	gct	gtc
ccc	ctc	caa	aaa	gag
ctg				452
Val	Gly	Pro	Pro	Leu
Pro	Gln	Glu	Ala	Val
Pro	Leu	Gln	Lys	Glu
Leu				
	105	110	115	
ccc	tct	ctc	cag	cac
ccc	aat	gaa	cag	aag
gaa	gga	acg	cca	gct
cca				500
Pro	Ser	Leu	Gln	His
Pro	Asn	Glu	Gln	Lys
Glu	Gly	Thr	Pro	Ala
Pro				
	120	125	130	
ttt	ggg	gac	cag	agc
cat	cca	gaa	cct	gag
tcc	tgg	aat	gca	gcc
cag				548
Phe	Gly	Asp	Gln	Ser
His	Pro	Glu	Pro	Glu
Ser	Trp	Asn	Ala	Ala
Gln				
	135	140	145	
cac	tgc	caa	cag	gac
cgg	tcc	caa	ggg	ggc
tgg	ggc	cac	cgg	ctg
gat				596
His	Cys	Gln	Gln	Asp
Arg	Ser	Gln	Gly	Gly
Trp	Gly	His	Arg	Leu
Asp				
	150	155	160	165
ggc	ttc	ccc	cct	ggg
cgg	cct	tct	cca	gac
aat	ctg	aac	caa	atc
tgc				644
Gly	Phe	Pro	Pro	Gly
Arg	Pro	Ser	Pro	Asp
Asn	Leu	Asn	Gln	Ile
Cys				
	170	175	180	
ctt	cct	aac	cgt	cag
cat	gtg	gta	tat	ggt
ccc	tgg	aac	cta	cca
cag				692
Leu	Pro	Asn	Arg	Gln
His	Val	Val	Tyr	Gly
Pro	Trp	Asn	Leu	Pro
Gln				
	185	190	195	

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740
 Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
 200 205 210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788
 Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
 215 220 225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836
 Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
 230 235 240 245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884
 Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
 250 255 260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932
 Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
 265 270 275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980
 His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
 280 285 290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028
 Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
 295 300 305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076

Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu

310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124

Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu

330 335 340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172

Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys

345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220

Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu

360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268

Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser

375 380 385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390 395 400 405

gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu

410 415 420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

384/735

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

430

435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440

445

450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455

460

465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470

475

480

485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490

495

500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

385/735

535

540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

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15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20

25

30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35

40

45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50

55

60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65

70

75

80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85

90

95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245 250 255
387/735

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu

260

265

270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln

275

280

285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro

290

295

300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser

305

310

315

320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu

325

330

335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly

340

345

350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys

355

360

365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys

370

375

380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala

385

390

395

400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg

388/735

405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu

420 425 430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435 440 445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500 505 510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

515 520 525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

530 535 540

<210> 112

<211> 1810

389/735

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102).. (1721)

<400> 112

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gaggaccac ctctgagtgt ccagtgtca gttgcccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

1

5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

60

65

390/735

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
 Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
 70 75 80 85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404
 Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
 90 95 100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452
 Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
 105 110 115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500
 Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
 120 125 130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548
 Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
 135 140 145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596
 His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
 150 155 160 165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644
 Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
 170 175 180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
185 190 195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
200 205 210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
215 220 225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
230 235 240 245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
250 255 260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
265 270 275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
280 285 290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028
392/735

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
 295 300 305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076
 Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
 310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124
 Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
 330 335 340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172
 Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
 345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220
 Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
 360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268
 Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
 375 380 385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316
 Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
 390 395 400 405

gac egg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364
 Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu
 393/735

410	415	420	
atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat			1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His			
425	430	435	
att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca			1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro			
440	445	450	
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc			1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile			
455	460	465	
aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc			1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu			
470	475	480	485
tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc			1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile			
490	495	500	
aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc			1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala			
505	510	515	
aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc			1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser			
520	525	530	
394/735			

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccaccctgc tgaacactca ttacactaaa cacctcttg 1810

<210> 113

<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala

1

5

10

15

Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe

20

25

30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35

40

45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50

55

60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu

65

70

75

80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro

245

250

255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser

260

265

270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu

275

280

285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln

290

295

300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met

305

310

315

320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp

325

330

335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu

340

345

350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser

355

360

365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile

370

375

380

<210> 114

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201).. (1346)

<400> 114

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aacagcagcg gagttttaaa ctttaaatag acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggcg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

5

10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

20

25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

30

35

40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

398/735

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

45

50

55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

60

65

70

75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu

80

85

90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn

95

100

105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val

110

115

120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile

125

130

135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

140

145

150

155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713

Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

399/735

160	165	170	
atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc	761		
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys			
175	180	185	
aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc	809		
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro			
190	195	200	
acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg	857		
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val			
205	210	215	
tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc	905		
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly			
220	225	230	235
gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt	953		
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser			
240	245	250	
ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat	1001		
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr			
255	260	265	
ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct	1049		
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro			
270	275	280	
400/735			

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097

Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

285

290

295

aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca 1145

Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala

300

305

310

315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193

Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320

325

330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241

Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

335

340

345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289

Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

350

355

360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337

Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

365

370

375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

380

ggagaagaaa aaaggtgctg tagaaagtc accaggtgtt aattttgatc cggaggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agaggaggag gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggtg 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata ttaacaatc 2166

acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga ttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

tctcatggat ttttgtgggtg tgggccaata tgggtgtttac attatataat tcctgctgtg 2346

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atactggttt tgtaattat gattctttat tttctctcct ttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcttttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaattttagt actgtaaaca ggcttttagtc attaattgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactgggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttatth ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcac gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttggt tgacattcca tgtaaaacta cggatcatgtt cagcttcatt gcatgtaatg 3006

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tttagtat 3074

<210> 115

<211> 382

<212> PRT

<213> Homo sapiens

<400> 115

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe

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Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35 40 45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50 55 60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu

65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val

85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu

100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys

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115 120 125
Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140
Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160
Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175
Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190
Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205
Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
210 215 220
Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225 230 235 240
Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
245 250 255
Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
290 295 300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
370 375 380

<210> 116

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201).. (1346)

<400> 116

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attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggcg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

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10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

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25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

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gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

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55

ggc tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

60

65

70

75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu

80

85

90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn

95

100

105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val

110

115

120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile

125

130

135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

140

145

150

155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713

Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

160

165

170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761

Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys

175

180

185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809

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Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro
190 195 200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val
205 210 215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly
220 225 230 235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser
240 245 250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr
255 260 265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
270 275 280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
285 290 295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala
409/735

300 305 310 315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
320 325 330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
335 340 345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
350 355 360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
365 370 375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386
Leu Glu Ile
380

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ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626
410/735

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

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ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

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tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

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cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

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cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

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<211> 398

<212> PRT

<213> Homo sapiens

<400> 117

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20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser

50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser

65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg

100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn

115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe

130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala

145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn

165

170

175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val

180

185

190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu

195

200

205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr

210

215

220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala

225

230

235

240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu

245

250

255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr

260

265

270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg

275

280

285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro

290

295

300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg

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305

310

315

320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr

325

330

335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu

340

345

350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355

360

365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

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Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

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<210> 118

<211> 2054

<212> DNA

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<220>

<221> CDS

<222> (76).. (1269)

<400> 118

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415/735

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met.

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175

180

185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser

190

195

200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu

205

210

215

220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783
417/735

Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
 225 230 235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831
 Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
 240 245 250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879
 Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
 255 260 265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927
 Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
 270 275 280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975
 Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
 285 290 295 300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023
 Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
 305 310 315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071
 Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
 320 325 330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119
 Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
 418/735

335 340 345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350 355 360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

365 370 375 380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385 390 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319
Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

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cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

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actcacctac tcatac 2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

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Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala

20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35 40 45

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Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser

50

55

60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser

65

70

75

80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

85

90

95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg

100

105

110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn

115

120

125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe

130

135

140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala

145

150

155

160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn

165

170

175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val

180

185

190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu

421/735

195 200 205
Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
210 215 220
Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225 230 235 240
His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
245 250 255
Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
260 265 270
Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
275 280 285
Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
290 295 300
Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305 310 315 320
Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
325 330 335
Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355

360

365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

370

375

380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385

390

395

<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 120

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Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu

15

20

25

423/735

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Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

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35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175

180

185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser

190

195

200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu

205

210

215

220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr

225

230

235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys

240

245

250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879

425/735

Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu

255

260

265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927

Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg

270

275

280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975

Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser

285

290

295

300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023

Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu

305

310

315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071

Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly

320

325

330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119

Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp

335

340

345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167

Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350

355

360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215

Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

426/735

365

370

375

380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263

Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385

390

395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319

Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gcccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatgt cccctgcct gtctttccag catccactct 1679

ccctgtcct cctgggggca tatctcagtc aggcagcggc ttctgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccgggt aagtaaagag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct cttagagctgt cttgtcccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatac 2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu

20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val

50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp

65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

428/735

85

90

95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu

100

105

<210> 122

<211> 1546

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89).. (412)

<400> 122

actaggcaga gccgtggaac cgccgccagg tcgctgttgg tccacgccgc ccgtcgcgcc 60

gcccgcgccgc tcagcgtccg ccgccgcc atg gga gtg cag gtg gaa acc atc 112

Met Gly Val Gln Val Glu Thr Ile

1

5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160

Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val

10

15

20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208

Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser

25

30

35

40

429/735

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256

Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val

45

50

55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304

Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg

60

65

70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352

Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His

75

80

85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400

Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu

90

95

100

cta aaa ctg gaa tgacaggaat ggccctcctcc cttagctccc tgttcttgga 452

Leu Lys Leu Glu

105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttcctct tcccctttct cctcgtatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatattt gttttcattt tgggggtgaag 692

attcagtttc agtcttttgg atataggttt ccaattaagt acatgggtcaa gtattaacag 752

cacaagtggg aggttaacat tagaatagga attggtgttg gggggggggg ttgcaagaat 812

atattatttt aattttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc 872

tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt 932

gagagatgtc tttgggttaa attaaaagcc ctacctaaaa ctgagggtggg gatggggaga 992

gcctttgcct ccaccattcc caccaccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcatgttcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc agggacctct 1112

gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa ctttccaagc tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtga agccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggcatcgc agcttcagca 1352

tctcctgttt ttgatgctt ggctccctct gctgatctca gtttcctggc ttttcctccc 1412

tcagccccct ctcacccctt tgctgtcctg tgtagtgatt tggtagagaa tcgttgctgc 1472

acccttcccc cagcaccatt tatgagtcctc aagttttatt attgcaataa aagtgcctta 1532

tgccggcttt tctc 1546

<210> 123

<211> 679

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly
1 5 10 15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala
20 25 30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe
35 40 45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile
50 55 60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys
65 70 75 80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn
85 90 95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly
100 105 110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
115 120 125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala
130 135 140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met
145 150 155 160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu
165 170 175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro
180 185 190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile
195 200 205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
210 215 220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
225 230 235 240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
245 250 255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
260 265 270
433/735

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser

275

280

285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala

290

295

300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys

305

310

315

320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val

325

330

335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val

340

345

350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn

355

360

365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp

370

375

380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val

385

390

395

400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn

405

410

415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser

434/735

420	425	430
Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu		
435	440	445
Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr		
450	455	460
Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile		
465	470	475
480		
Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser		
485	490	495
Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser		
500	505	510
Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe		
515	520	525
Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala		
530	535	540
Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr		
545	550	555
560		
Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu		
565	570	575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
580 585 590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
595 600 605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
610 615 620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
625 630 635 640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
645 650 655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
660 665 670

Arg Tyr Val Ile Leu Arg Met
675

<210> 124

<211> 2916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81).. (2117)

<400> 124

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aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala

1 5 10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

15 20 25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

30 35 40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

45 50 55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val

60 65 70 75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353

Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp

80 85 90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc 401

Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val

95

100

105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449

Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu

110

115

120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497

Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly

125

130

135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545

Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu

140

145

150

155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593

Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile

160

165

170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641

Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys

175

180

185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc 689

Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala

190

195

200

tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg 737

438/735

Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro

205

210

215

ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg 785

Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser

220

225

230

235

gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt 833

Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys

240

245

250

ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct 881

Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser

255

260

265

gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa 929

Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu

270

275

280

gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct 977

Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser

285

290

295

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga 1025

Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg

300

305

310

315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag 1073

Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu

439/735

320	325	330	
agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc	1121		
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr			
335	340	345	
gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt	1169		
Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser			
350	355	360	
caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac	1217		
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His			
365	370	375	
acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta	1265		
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu			
380	385	390	395
cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc	1313		
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro			
400	405	410	
tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc	1361		
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly			
415	420	425	
atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa	1409		
Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu			
430	435	440	
440/735			

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att 1457

Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile

445

450

455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac 1505

Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His

460

465

470

475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt 1553

Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly

480

485

490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat 1601

Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp

495

500

505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc 1649

Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala

510

515

520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att 1697

Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile

525

530

535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct 1745

Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser

540

545

550

555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt 1793
Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly

560

565

570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg 1841
Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met

575

580

585

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa 1889
Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu

590

595

600

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc 1937
Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro

605

610

615

atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg 1985
Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp

620

625

630

635

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt 2033
Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe

640

645

650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc 2081
Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala

655

660

665

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt 2127

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Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga 2187

atgattacag tgtaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgctataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggctc ctttccttc tgggctgtga 2367

attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttat 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac ttgggcaag 2847

ttaaatggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agtttttag

2916

<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala

1 5 10 15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20 25 30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35 40 45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50 55 60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro

65 70 75 80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp

85 90 95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln

100 105 110

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Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu

115

120

125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly

130

135

140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser

145

150

155

160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr

165

170

175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr

180

185

190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu

195

200

205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp

210

215

220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala

225

230

235

240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys

245

250

255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu

445/735

260

265

270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met

275

280

285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81).. (944)

<400> 126

tcaacgcctg cctcccctcg agcgtcctca gcgcagccgc cgcccgcgga gccagcacga 60

acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln

1

5

10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161

Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln

15

20

25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209

Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr

30

35

40

446/735

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257

Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val

45

50

55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305

Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala

60

65

70

75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353

Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln

80

85

90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401

Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr

95

100

105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc 449

Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg

110

115

120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497

Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly

125

130

135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545

Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu

140

145

150

155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593

Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn

160

165

170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641

Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn

175

180

185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689

Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala

190

195

200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737

Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu

205

210

215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785

Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly

220

225

230

235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833

Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu

240

245

250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881

Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

260

265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929

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Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val

270

275

280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984

Gly Leu Tyr Ala Met

285

ccggtggaag gccttctttc tagagagggga attctcttgg ctggcttcct taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcattctccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acaccctaatt gtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttggtgc ttgtgttttt gtcttatattt tgttggagcc actctgttcc tggctcagcc 1404

tcaaatagcag tatttttgtt gtgttctgtt gtttttatag cagggttggg gtggtttttg 1464

agccatgcgt ggggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg 1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1 5 10 15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

20 25 30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35 40 45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50 55 60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65 70 75 80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

85 90 95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

100 105 110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys

115 120 125

Ile Lys Cys Val Ala Phe Asp

130

135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50).. (454)

<400> 128

cttctgacag ctggtgogcc tgcccgggaa catcctcctg gactcaatc atg gct tgt 58

Met Ala Cys

1

ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106

Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg

5

10

15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154

Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu

20

25

30

35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202

Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn

40

45

50

451/735

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250
Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
55 60 65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298
Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
70 75 80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346
Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
85 90 95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394
Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
100 105 110 115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442
Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys
120 125 130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494
Val Ala Phe Asp
135

ctctgctccc ctg 507

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn

1 5 10 15

Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn

20 25 30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

35 40 45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

50 55 60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65 70 75 80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr

85 90 95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu

100 105 110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys

115 120 125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
130 135 140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
145 150 155 160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
165 170 175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
180 185 190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
195 200 205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
210 215 220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
225 230 235 240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
245 250 255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
260 265 270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
275 280 285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys

290

295

300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val

305

310

315

320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala

325

330

335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe

340

345

350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp

355

360

365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln

370

375

380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp

385

390

395

400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu

405

410

415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe

420

425

430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn

455/735

435 440 445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile
450 455 460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp
465 470 475 480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu
485 490 495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser
500 505 510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr
515 520 525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn
530 535 540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly
545 550 555 560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln
565 570 575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln
580 585 590

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Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn

595

600

605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe

610

615

620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn

625

630

635

640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg

645

650

655

Leu Arg Ile Ser Glu Lys

660

<210> 130

<211> 2251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74).. (2059)

<400> 130

cttggtgga cagtttgtga aactgtgttg ccgggcaact ggacatcctt ttgttcaata 60

tcagtgggtc aaa atg aat aaa gag att cca aat gga aat aca tca gag 109

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Met	Asn	Lys	Glu	Ile	Pro	Asn	Gly	Asn	Thr	Ser	Glu	
1					5						10	
ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt												157
Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys												
15					20						25	
cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg												205
Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu												
30					35						40	
gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc												253
Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val												
45					50						55	60
tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg												301
Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu												
65											70	75
atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct												349
Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro												
80											85	90
att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag												397
Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu												
95											100	105
acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga												445
Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly												
												458/735

110 115 120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag 493
Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys
125 130 135 140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act 541
Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr
145 150 155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca 589
Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr
160 165 170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat 637
Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn
175 180 185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg 685
Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val
190 195 200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca 733
Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser
205 210 215 220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt 781
Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe
225 230 235

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tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829
Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly
240 245 250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877
His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala
255 260 265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925
Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu
270 275 280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973
Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp
285 290 295 300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021
Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp
305 310 315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069
Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln
320 325 330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117
Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile
335 340 345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165
Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr

350

355

360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213
Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr

365

370

375

380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261
Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg

385

390

395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309
Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu

400

405

410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357
Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met

415

420

425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405
Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala

430

435

440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro

445

450

455

460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501
461/735

Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp

465

470

475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549

Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr

480

485

490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597

Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr

495

500

505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645

Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val

510

515

520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693

Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys

525

530

535

540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741

Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His

545

550

555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789

Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn

560

565

570

ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837

Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr

462/735

575 580 585

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885
His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly
590 595 600

aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933
Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr
605 610 615 620

cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981
Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe
625 630 635

agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029
Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser
640 645 650

ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa 2079
Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys
655 660

gtagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139

gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc 2199

aggactttga gatgttgaaa ttacattatt taattacaga cttcctcttt ct 2251

<210> 131

<211> 824

<212> PRT

<213> Homo sapiens

<400> 131

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala
1 5 10 15

Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg
20 25 30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala
35 40 45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg
50 55 60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
65 70 75 80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
85 90 95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
100 105 110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
115 120 125

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Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val

130

135

140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp

145

150

155

160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile

165

170

175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val

180

185

190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val

195

200

205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu

210

215

220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro

225

230

235

240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro

245

250

255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys

260

265

270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr

465/735

275 280 285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
290 295 300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305 310 315 320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
325 330 335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
340 345 350

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
355 360 365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
370 375 380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385 390 395 400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
405 410 415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
420 425 430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
435 440 445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
450 455 460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465 470 475 480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
485 490 495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
500 505 510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
515 520 525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
530 535 540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545 550 555 560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
565 570 575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
580 585 590
467/735

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe

595

600

605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu

610

615

620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp

625

630

635

640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser

645

650

655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu

660

665

670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu

675

680

685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu

690

695

700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly

705

710

715

720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro

725

730

735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser

468/735

740

745

750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro

755

760

765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp

770

775

780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg

785

790

795

800

Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser

805

810

815

Asp Arg Leu Arg Ile Ser Glu Lys

820

<210> 132

<211> 2828

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (165)..(2636)

<400> 132

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469/735

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gggcgggagg gagccccggc agtcgggggt cgccggcgag ggcc atg tcg ctg ttg 176

Met Ser Leu Leu

1

ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224

Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro

5 10 15 20

ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg 272

Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro

25 30 35

ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc ccg 320

Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg

40 45 50

ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc 368

Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg

55 60 65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416

Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro

70 75 80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464

Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly

470/735

85	90	95	100
tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act 512			
Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr			
105	110	115	
gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac 560			
Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn			
120	125	130	
cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc 608			
Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys			
135	140	145	
cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat 656			
Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn			
150	155	160	
aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg 704			
Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val			
165	170	175	180
cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc 752			
His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe			
185	190	195	
acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca 800			
Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro			
200	205	210	
471/735			

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa 848

Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln

215

220

225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg 896

Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu

230

235

240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg 944

Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp

245

250

255

260

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg 992

Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met

265

270

275

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta 1040

Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val

280

285

290

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088

Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile

295

300

305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136

Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn

310

315

320

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg 1184
 Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala
 325 330 335 340

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac 1232
 Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His
 345 350 355

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta 1280
 Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu
 360 365 370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa 1328
 Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu
 375 380 385

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag 1376
 Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys
 390 395 400

gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt 1424
 Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe
 405 410 415 420

ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct 1472
 Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser
 425 430 435

gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa 1520
 473/735

Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys

440

445

450

gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat 1568

Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn

455

460

465

gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc 1616

Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala

470

475

480

aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa 1664

Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu

485

490

495

500

atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa 1712

Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys

505

510

515

gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt 1760

Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val

520

525

530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808

Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu

535

540

545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856

Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile

474/735

550	555	560	
cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg			1904
Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp			
565	570	575	580
gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt			1952
Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys			
585	590	595	
ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg			2000
Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met			
600	605	610	
atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt			2048
Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys			
615	620	625	
gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa			2096
Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys			
630	635	640	
gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca			2144
Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser			
645	650	655	660
aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa			2192
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln			
665	670	675	
475/735			

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac 2240
Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr
680 685 690

tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg 2288
Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly
695 700 705

aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag 2336
Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
710 715 720

act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct 2384
Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
725 730 735 740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca 2432
Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro
745 750 755

ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca 2480
Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr
760 765 770

cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca 2528
Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser
775 780 785

agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca 2576

Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro

790

795

800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624

Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg

805

810

815

820

att tct gaa aaa tgacctcctt gtttttgaaa gttagcataa ttttagatgc 2676

Ile Ser Glu Lys

ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

gtagagaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796

ttacattatt taattacaga cttcctcttt ct 2828

<210> 133

<211> 919

<212> PRT

<213> Homo sapiens

<400> 133

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn Glu Thr

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15

Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser

20

25

30

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Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys

35

40

45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp

50

55

60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys

65

70

75

80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu

85

90

95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile

100

105

110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu

115

120

125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu

130

135

140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr

145

150

155

160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe

165

170

175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr

478/735

180	185	190
Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly		
195	200	205
Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg		
210	215	220
Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu		
225	230	235
240		
Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr		
245	250	255
Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr		
260	265	270
Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly		
275	280	285
Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala		
290	295	300
Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu		
305	310	315
320		
Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro		
325	330	335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr
340 345 350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser
355 360 365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly
370 375 380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala
385 390 395 400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
405 410 415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
420 425 430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
435 440 445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
450 455 460

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys
465 470 475 480

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
485 490 495
480/735

Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln

500

505

510

Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala

515

520

525

Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile

530

535

540

Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile

545

550

555

560

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr

565

570

575

Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln

580

585

590

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser

595

600

605

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His

610

615

620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala

625

630

635

640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp

481/735

645	650	655
Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala		
660	665	670
Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala		
675	680	685
Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg		
690	695	700
Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala		
705	710	715
720		
Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp		
725	730	735
Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu		
740	745	750
Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp		
755	760	765
Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile		
770	775	780
Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp		
785	790	795
800		

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val

805 810 815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser

820 825 830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val

835 840 845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu

850 855 860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe

865 870 875 880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys

885 890 895

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr

900 905 910

Ser Ser Ser Phe Leu Glu Val

915

<210> 134

<211> 3612

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (427).. (3183)

<400> 134

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gagcaggctc ccgcctcgca ccgtgcccc gcgagcagct cctcttctcc cgaggcgcgc 180
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ggtgacagcc tgggattccg ggggcttctc ttccttgtec tctcctctc ctctctattc 360
ccagtgtggc cgtggctgac actaaagact ttgtagccat caaccgagt gcagtttcga 420
tggaat atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat 468
Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn
1 5 10
gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca 516
Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro
15 20 25 30
gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta 564
484/735

Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu

35

40

45

aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag 612

Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu

50

55

60

ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag 660

Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln

65

70

75

ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt 708

Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser

80

85

90

gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata 756

Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile

95

100

105

110

ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa 804

Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys

115

120

125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg 852

Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val

130

135

140

cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900

Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly

485/735

145 150 155
gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc 948
Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg
160 165 170
ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt 996
Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly
175 180 185 190
gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act 1044
Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr
195 200 205
aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg 1092
Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu
210 215 220
gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat 1140
Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn
225 230 235
tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca 1188
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro
240 245 250
aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc 1236
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser
255 260 265 270

ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta 1284

Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu

275

280

285

ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct 1332

Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala

290

295

300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta 1380

Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu

305

310

315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag 1428

Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys

320

325

330

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat 1476

Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp

335

340

345

350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt 1524

Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe

355

360

365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa 1572

Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln

370

375

380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac 1620
Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn

385

390

395

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct 1668
Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala

400

405

410

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta 1716
Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu

415

420

425

430

att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac 1764
Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr

435

440

445

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct 1812
Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala

450

455

460

gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt 1860
Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe

465

470

475

atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag 1908
Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln

480

485

490

agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac 1956
488/735

Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr
 495 500 505 510

caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct 2004
 Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala
 515 520 525

ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg 2052
 Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val
 530 535 540

gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100
 Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr
 545 550 555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag 2148
 Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln
 560 565 570

gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act 2196
 Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr
 575 580 585 590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag 2244
 Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln
 595 600 605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca 2292
 Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro
 489/735

610	615	620	
agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt 2340			
Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val			
625	630	635	
gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct 2388			
Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala			
640	645	650	
gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa 2436			
Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys			
655	660	665	670
gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg 2484			
Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met			
675	680	685	
tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc 2532			
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe			
690	695	700	
gtt aga ttc cag ctg agc acg agt ata gca gca tta act tta atc tca 2580			
Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser			
705	710	715	
ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att 2628			
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile			
720	725	730	
490/735			

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga 2676
Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly
735 740 745 750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg 2724
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp
755 760 765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca 2772
Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser
770 775 780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta 2820
Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu
785 790 795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc 2868
Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
800 805 810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc 2916
Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
815 820 825 830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964
Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
835 840 845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012
Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro

850

855

860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060
Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu

865

870

875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att 3108
Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile

880

885

890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt 3156
Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser

895

900

905

910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattatatt 3203
Ser Thr Ser Ser Ser Phe Leu Glu Val

915

tatttgcaaa ctaggaattg cagtctgagg atcatttaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaa tgaacattaa tgtaaagac 3323

ttaagacttt aacctgctgg cagtcccaaa tgaattatg caactttgat atcatattcc 3383

ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttatatt 3443

aattaaaaag gcaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaaata 3503

cactatctat cttagataga tatatTTTTT tttatTTTTa aatattgtac tatttatggt 3563

ggtggggcctt tcttactaat acacaaataa atttaaatcat ttcaaaggc 3612

<210> 135

<211> 382

<212> PRT

<213> Homo sapiens

<400> 135

Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln

1 5 10 15

Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp

20 25 30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser

35 40 45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50 55 60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr

65 70 75 80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn

85 90 95

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Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met

100

105

110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr

115

120

125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys

130

135

140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe

145

150

155

160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln

165

170

175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala

180

185

190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys

195

200

205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile

210

215

220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly

225

230

235

240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser

494/735

245 250 255
Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val
260 265 270
Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu
275 280 285
Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys
290 295 300
Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile
305 310 315 320
Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr
325 330 335
Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala
340 345 350
Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr
355 360 365
Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp
370 375 380

<210> 136

<211> 2467

495/735

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (444)..(1589)

<400> 136

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tctagacagc tgaggcgcga aagcgatgag tcctcggctc ttctcctcc ttctccggga 180
cccgctctct gcctccctct ccaacgcccg gatgatctga gccgcgaggg cgccgacagc 240
cgggggccccg gacgcagccc ggctcctccc ctctccgcc ccttccccag cctgacctgg 300
cccgcgctg cagcggtgac ccctcccccg gctgccgccg tcgccgccgc ggtgaccccc 360
tccccggctg ccgccgccgc cgctcggcc gaccaggac ctgccgcct gcggctgctc 420
cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473
Met Gly Ala Phe Leu Asp Lys Pro Lys Met
1 5 10
gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta 521
Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu
15 20 25
496/735
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agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569

Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30

35

40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617

Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45

50

55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665

Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

60

65

70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713

Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

75

80

85

90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761

Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

95

100

105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809

Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala

110

115

120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat 857

Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

125

130

135

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905
Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn
140 145 150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953
Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu
155 160 165 170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001
Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg
175 180 185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049
Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr
190 195 200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097
Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu
205 210 215

cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145
Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile
220 225 230

atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc 1193
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu
235 240 245 250

tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa 1241
498/735

Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys

255

260

265

gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac 1289

Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp

270

275

280

aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg 1337

Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser

285

290

295

cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc 1385

Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys

300

305

310

aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta 1433

Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu

315

320

325

330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481

Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro

335

340

345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529

Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr

350

355

360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577

Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

499/735

365

370

375

gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc 1629

Asp Asp Met Trp

380

aaaggagagt acagctcaac tttgttgaaa cttttaacat ccatcctcaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaaatt cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catatttaatt tatgaactgc tttaaatcac 1929

tatcaaagtt acaagaaatg tttggcttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcatggt gtgtttggac ttggggtttg aacagggaga gcagcagcca tgcagctac 2049

acgctcaaatt gtgcagatga ttatggaaaa taacctcaaa atcttataaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaatgt tcttggtagg ggagttggca ttgttgataa 2169

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caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137

<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val

1 5 10 15

Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp

20 25 30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu

35 40 45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val

50 55 60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg

65 70 75 80

Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn

85 90 95

501/735

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser

100

105

110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser

115

120

125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met

130

135

140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala

145

150

155

160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser

165

170

175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr

180

185

190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln

195

200

205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln

210

215

220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro

225

230

235

240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln

502/735

245 250 255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln

260 265 270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr

275 280 285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln

290 295 300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly

305 310 315 320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro

325 330 335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln

340 345 350

Pro Gly Pro Gly Tyr Arg

355

<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11).. (1084)

<400> 138

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10

gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca 97

Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr

15

20

25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata 145

Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile

30

35

40

45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca 193

Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser

50

55

60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa 241

Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

65

70

75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct 289

Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

80

85

90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag 337

Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys

95

100

105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca 385

Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala

110

115

120

125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa 433

Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys

130

135

140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca 481

Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro

145

150

155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct 529

Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala

160

165

170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca 577

Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro

175

180

185

cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac 625

Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr

190

195

200

205

cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag 673

505/735

Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln
210 215 220

cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag 721
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln
225 230 235

act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca 769
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro
240 245 250

act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg 817
Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu
255 260 265

cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa 865
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
270 275 280 285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct 913
Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro
290 295 300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961
Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro
305 310 315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009
Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro
506/735

320

325

330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc 1057

Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly

335

340

345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc 1104

Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

350

355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164

ttgaagaagt tcagaaattt aaaagcagag cattttttat gatatcattg ttggtggtta 1224

ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tccctgctta 1284

aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtgattga 1344

cttgactttc tagcttcctt tgtccggagg atattaaaat gctaggggtga ggtttagcca 1404

tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464

gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc 1519

<210> 139

<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

1 5 10 15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr

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Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu

35 40 45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp

50 55 60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys

65 70 75 80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro

85 90 95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu

100 105 110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu

115 120 125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg

130 135 140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
145 150 155 160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
165 170 175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
180 185 190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
195 200 205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
210 215 220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
225 230 235 240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
245 250 255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
260 265 270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
275 280 285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
290 295 300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr

305 310 315 320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr

325 330 335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala

340 345 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr

355 360 365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe

370 375 380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

385 390 395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1206)

<400> 140

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Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu

1

5

10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99

Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His

15

20

25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147

Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val

30

35

40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195

Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys

45

50

55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243

Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser

60

65

70

75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291

Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn

80

85

90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339

Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg

95

100

105

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gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg 387

Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu

110

115

120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat 435

Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp

125

130

135

act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa 483

Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys

140

145

150

155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta 531

Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu

160

165

170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta 579

Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu

175

180

185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt 627

Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg

190

195

200

tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca 675

Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro

205

210

215

cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa 723

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Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln
 220 225 230 235

gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca 771
 Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala
 240 245 250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819
 Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln
 255 260 265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867
 Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln
 270 275 280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915
 Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala
 285 290 295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963
 Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
 300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011
 Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
 320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059
 Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
 513/735

335 340 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107
Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro

350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155
Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg

365 370 375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat 1203
Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr

380 385 390 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256
Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

cattttttat gataatcattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga 1436

acactactct tacatgtata aagtgattga cttgactttc tagcttcctt tgtccggagg 1496

atattaaaat gctaggggtga ggtttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616

taggttaata aagatgattg aatcc

1641

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<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1 5 10 15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr

20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly

65 70 75 80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly

85 90 95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val

100 105 110

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Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe

115

120

125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr

130

135

140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile

145

150

155

160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe

165

170

175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro

180

185

190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser

195

200

205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile

210

215

220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe

225

230

235

240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly

245

250

255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln

516/735

260 265 270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala

275 280 285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu

290 295 300

Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His

305 310 315 320

Val Gln Thr

<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)..(1040)

<400> 142

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gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

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1	5	10	
gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt			158
Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu			
15	20	25	
cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt			206
Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe			
30	35	40	45
gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac			254
Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His			
50	55	60	
ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg			302
Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg			
65	70	75	
cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc			350
Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe			
80	85	90	
cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat			398
Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp			
95	100	105	
ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc			446
Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg			
110	115	120	125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494
 Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln
 130 135 140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542
 Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro
 145 150 155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590
 Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly
 160 165 170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638
 Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro
 175 180 185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686
 Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro
 190 195 200 205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734
 Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg
 210 215 220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782
 Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn
 225 230 235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac 830
Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn

240

245

250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc 878
Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val

255

260

265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc 926
Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu

270

275

280

285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg 974
Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu

290

295

300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag 1022
Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln

305

310

315

ctg acc cat gtg cag aca taggcggcctt cctggccctg gggccggggg 1070
Leu Thr His Val Gln Thr

320

ctgggggtgtg gggcagtcctg ggtcctctca tcattcccccac ttcccaggcc cagcctttcc 1130

aaccctgcct gggatctggg cttaaatgca gaggccatgt ccttgtcttg tcctgcttct 1190

ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag 1250

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cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310

agagggggagg agtgggcagt gaagatgaag ccccatgctc agtcccctcc catccccac 1370

gcagctccac ccagtcacca agccaccagc tgtctgctcc tgggtgggagg tggcctcctc 1430

agccccctct ctctgacctt taacctcact ctacacttgc accgtgcacc aacccttcac 1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

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35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

85 90 95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His

100 105 110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe

115 120 125

Leu Gln Pro Leu Met His Cys Val

130 135

<210> 144

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225).. (632)

<400> 144

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ggcgcccttc gtcccgggtcc catcctcgcc gcgtccagc acctctgaag tttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55

60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

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Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70

75

80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85

90

95

100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572

Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser

105

110

115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620

Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu

120

125

130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672

Met His Cys Val

135

ttgttaatta gtgacatagt aacatctgta gcagctgggt agtaaacctc atgtgggggt 732

gggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac 792

atttttcctg ttttaaattc taggatagat ttaacatcc tttgcgggtcc cagtccaagg 852

taggctgggtg tcatagtctt ctactocta atccatgacc actgtttttt tcctatttat 912

atcaccaggt agcctactga gttaatatat aagttgtcaa tagataagtg tccctgtttt 972

gtggcataat ataactgaat ttcattgagaa gatttattcc accaggggta tttcagcttt 1032

gaaaccaaatt ctgtgtatct aataactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212

gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe

20 25 30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln

35 40 45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg

50 55 60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro

65 70 75 80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu

85 90 95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser

100 105 110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu

115 120 125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu

130 135 140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met

145 150 155 160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp

165 170 175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val

180 185 190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu

195 200 205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp

210 215 220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile

225 230 235 240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala

245 250 255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu

260 265 270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe

275 280 285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe

290 295 300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys

305 310 315 320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser

325 330 335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile

340 345 350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met

355 360 365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys

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370

375

380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile
385 390 395 400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala
405 410 415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu
420 425 430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr
435 440 445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala
450 455 460

Ala Ser Gly Ile
465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379).. (1782)

<400> 146

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta tttaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gaggaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcatcgctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly

1 5 10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459

Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys

15 20 25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc 507

Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe

30 35 40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val

45 50 55

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tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603
 Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala
 60 65 70 75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651
 His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys
 80 85 90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699
 Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe
 95 100 105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747
 Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg
 110 115 120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795
 Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile
 125 130 135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843
 Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys
 140 145 150 155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891
 Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile
 160 165 170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val
175 180 185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile
190 195 200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met
205 210 215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083
Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu
220 225 230 235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag 1131
Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu
240 245 250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt 1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val
255 260 265

ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa 1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln
270 275 280

ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag 1275
531/735

Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu
285 290 295

ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac 1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr
300 305 310 315

ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt 1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser
320 325 330

ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac 1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His
335 340 345

tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg 1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu
350 355 360

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg 1515
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr
365 370 375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563
Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala
380 385 390 395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611
Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu
532/735

400 405 410

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc 1659
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser
415 420 425

aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt 1707
Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe
430 435 440

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
445 450 455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802
Ile Asn Asp Asn Ala Ala Ser Gly Ile
460 465

tgtttatcag ctttgcat ttc gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaa ataaaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t 1943

<210> 147

<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly
20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro
35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr
50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr
65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val
85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
100 105 110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
130 135 140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
145 150 155 160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
165 170 175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
180 185 190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
195 200 205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
210 215 220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp
225 230 235 240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
245 250 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg
260 265 270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile
275 280 285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu
290 295 300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg

305 310 315 320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg

325 330 335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu

340 345 350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser

355 360 365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val

370 375 380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val

385 390 395 400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu

405 410 415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys

420 425 430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys

435 440 445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile

536/735

450

455

460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376)..(1755)

<400> 148

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agaaaggagg cgaggaagga gggagtgtat gagaggagg agcaaaaagc tcaccctaaa 180

acatttatatt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgcctttct ggtgggaggc ttgattgctc cagggccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser

1

5

10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459

Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg

15

20

25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507

Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr

30

35

40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555

Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe

45

50

55

60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603

Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys

65

70

75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651

Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr

80

85

90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699

Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys

95

100

105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747

Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile

110

115

120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795

538/735

Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His

125 130 135 140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843

Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu

145 150 155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891

Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr

160 165 170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939

Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu

175 180 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987

Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile

190 195 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc 1035

Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly

205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083

Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu

225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131

His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys

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240	245	250	
caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac 1179			
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp			
255	260	265	
atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg 1227			
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp			
270	275	280	
act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct 1275			
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala			
285	290	295	300
gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt 1323			
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe			
305	310	315	
cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg 1371			
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met			
320	325	330	
agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419			
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys			
335	340	345	
ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467			
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe			
350	355	360	
540/735			

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile
365 370 375 380

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
385 390 395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611
Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
400 405 410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659
Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
415 420 425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707
Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
430 435 440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755
Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
445 450 455 460

tgagtcaaca aggcaacaca tgtttatcag ctttgcattt gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaatt 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc

1919

<210> 149

<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1 5 10 15

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65 70 75 80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100 105 110

542/735

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115

120

125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser

130

135

140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

145

150

155

160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165

170

175

Asp Arg His Lys Met Leu Ser

180

<210> 150

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120).. (668)

<400> 150

tacggctgcg agaagacgac agaaggggat taagaggag ggcggggaca actgggtctt 60

ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119

atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1

5

10

15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20

25

30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50

55

60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65

70

75

80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85

90

95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100

105

110

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gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115

120

125

gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser

130

135

140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

145

150

155

160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165

170

175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698

Asp Arg His Lys Met Leu Ser

180

ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc 758

tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctctttctcc ctaacttttag 818

aaatgttgta cttggctatt ttgattaggg aagagggatg tggctctctga tctccgttgt 878

cttcttgggt ctttggggtt gaaggagggg ggaaggcagg ccagaaggga atggagacat 938

tcgaggcggc ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 998

cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc ttcaggaact 1058

cagtgtctgg gaggaagca tggcccagca ttcagcatgt gttcctttct gcagtgggtc 1118

tttatcacca cctccctccc agccccagcg cctcagcccc agccccagct ccagccctga 1178

ggacagctct gatgggagag ctgggcccc tgagcccact gggctctcag ggtgcactgg 1238

aagctgggtg tcgtgtccc ctgtgcactt ctgcactgg ggcattggagt gccatgcat 1298

actctgctgc cggccccctc acctgcactt gaggggtctg ggcagtccct cctctcccca 1358

gtgtccacag tcaactgagc agacggctcg ttggaacatg agactcgagg ctgagcgtgg 1418

atctgaacac cacagcccct gtacttgggt tgctcttctg ccctgaactt cgttgtacca 1478

gtgcatggag agaaaatttt gtcctcttct cttagagttg tgtgtaaatc aaggaagcca 1538

tcattaaatt gttttatttc tctc 1562

<210> 151

<211> 2815

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (192).. (2387)

<400> 151

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cagccaggtc tgtgctgccg ccctccagca tctttgcagc aggggacgag gctgtgtggg 120

aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggcttcatt 180

ctcccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly

1

5

10

att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278

Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys

15

20

25

ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc 326

Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala

30

35

40

45

atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374

Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu

50

55

60

gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg 422

Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp

65

70

75

547/735

gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470
Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser
80 85 90

tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518
Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys
95 100 105

ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt 566
Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe
110 115 120 125

gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg 614
Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp
130 135 140

gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca 662
Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro
145 150 155

ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca 710
Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala
160 165 170

gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758
Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp
175 180 185

gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac	806
Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His	
190 195 200 205	
cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat	854
Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His	
210 215 220	
gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag	902
Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln	
225 230 235	
gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc	950
Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser	
240 245 250	
tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa	998
Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu	
255 260 265	
att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct	1046
Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro	
270 275 280 285	
gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc	1094
Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys	
290 295 300	
aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa	1142
549/735	

Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu
305 310 315

agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt 1190
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val
320 325 330

cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct 1238
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro
335 340 345

gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct 1286
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro
350 355 360 365

ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc 1334
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser
370 375 380

aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat 1382
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr
385 390 395

aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt 1430
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg
400 405 410

att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc 1478
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe
550/735

415 420 425

tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa 1526
Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln

430 435 440 445

gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc 1574
Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser

450 455 460

ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac 1622
Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn

465 470 475

agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca 1670
Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro

480 485 490

ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc 1718
Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu

495 500 505

cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag 1766
His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys

510 515 520 525

gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc 1814
Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg

530 535 540

551/735

tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag 1862

Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln

545

550

555

ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca 1910

Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr

560

565

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gcc tat gtc cat agc tat agg gcc tgg caa gca gag atg aac aaa ctt 1958

Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu

575

580

585

ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc 2006

Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser

590

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600

605

tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act 2054

Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr

610

615

620

cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca 2102

Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro

625

630

635

tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg 2150

Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu

640

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cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc 2198
Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser

655

660

665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc 2246
Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala

670

675

680

685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg 2294
Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly

690

695

700

gcc cag tca tct gat gac aag act gag tgt tcg gag aac ccc tgt atg 2342
Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met

705

710

715

ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag 2387
Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu

720

725

730

tgaccaggtt ggacccacc tagatggcta gaggacaag attggacttc acctgggtcc 2447

ttaaaatgat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta 2507

gcttgggctc ccacagtggc tattagtgg acccagcttg agacccaga ggcagggaag 2567

accacaccta taaatcaggc ctgggaaca tgcagaaacc ccatttgaac agactgtggg 2627

actccaatct gaatcctcta tgtggacaga ggatgatggg gccagaggca cctctgaggt 2687

553/735

gccctcagcg cagcctogta aacttcattc actgtgacac atgctgttca tagggtctct 2747

ctggggagga tgcggtcccg gggcacatag ggagggctct gtttttataa taaagttatt 2807

gacaactg 2815

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<212> PRT

<213> Mus musculus

<400> 152

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1 5 10 15

Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys Leu Gly Ser

20 25 30

Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu

35 40 45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu

50 55 60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met

65 70 75 80

Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val

85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser

100 105 110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln

115 120 125

Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys

130 135 140

Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser

145 150 155 160

His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg

165 170 175

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr

180 185 190

Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile

195 200 205

Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His

210 215 220

Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln

225 230 235 240

Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro

245

250

255

Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val

260

265

270

Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu

275

280

285

Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu

290

295

300

Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly

305

310

315

320

Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val Pro Val Gly

325

330

335

Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro Ala Gln Pro

340

345

350

Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro Leu Ser Ser

355

360

365

Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser Thr Ser Pro

370

375

380

Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val

556/735

385 390 395 400
Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu
 405 410 415
Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu
 420 425 430
Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile
 435 440 445
Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys
 450 455 460
Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr
465 470 475 480
Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys
 485 490 495
Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile
 500 505 510
Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn
 515 520 525
Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys
 530 535 540

Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala
545 550 555 560

Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val
565 570 575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala
580 585 590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly
595 600 605

Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe
610 615 620

Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro
625 630 635 640

Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val
645 650 655

Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro
660 665 670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val
675 680 685

Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser
690 695 700

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Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu

705

710

715

720

Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu

725

730

<210> 153

<211> 2544

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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agcttctgct gccggaggct gcaccacct gtgccc atg gcc tgc aca ggc cca 114

Met Ala Cys Thr Gly Pro

1

5

tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag 162

Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys

10

15

20

ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210
 Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln

25

30

35

ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258
 Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu

40

45

50

act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306
 Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala

55

60

65

70

cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354
 Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro

75

80

85

gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402
 Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu

90

95

100

ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac 450
 Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr

105

110

115

cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg 498
 Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly

120

125

130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg 546

560/735

Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly
 135 140 145 150

gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca 594
 Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro
 155 160 165

cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att 642
 Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile
 170 175 180

gac ggt gtt tcg gac tgg agc caa ggg tgc tcc ctg cga tcc act ggc 690
 Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly
 185 190 195

agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc 738
 Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr
 200 205 210

atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc 786
 Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu
 215 220 225 230

tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc 834
 Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly
 235 240 245

tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc 882
 Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala
 561/735

250 255 260

agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg 930
Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val

265 270 275

gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca 978
Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro

280 285 290

gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc 1026
Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly

295 300 305 310

ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc 1074
Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys

315 320 325

tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc 1122
Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr

330 335 340

tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca 1170
Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr

345 350 355

tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct 1218
Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala

360 365 370

cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg 1266
 His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser
 375 380 385 390

gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa 1314
 Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu
 395 400 405

cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc 1362
 His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro
 410 415 420

gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag 1410
 Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu
 425 430 435

ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta 1458
 Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu
 440 445 450

ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac 1506
 Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn
 455 460 465 470

caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc 1554
 Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val
 475 480 485

atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac 1602
Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp

490

495

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acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag 1650
Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln

505

510

515

atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag 1698
Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln

520

525

530

gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg 1746
Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg

535

540

545

550

gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg 1794
Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu

555

560

565

aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca 1842
Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala

570

575

580

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg 1890
Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly

585

590

595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc 1938
564/735

Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro
 600 605 610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg 1986
 Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro
 615 620 625 630

cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca 2034
 Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro
 635 640 645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc 2082
 Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala
 650 655 660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc 2130
 Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro
 665 670 675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac 2178
 Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His
 680 685 690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag 2226
 Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu
 695 700 705 710

gca gaa tgaccgcgtg tccttgccctg accacctggg gaacaccct ggaccaggc 2282
 Ala Glu

atcggccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtgggaagat 2342

gaggtcatct gccactttca ggacattgtc cgggagccct tcatttagga caaacgggc 2402

gcgatgatgc cctggctttc aggggtgtca gaactggata cggtggttac aattccaatc 2462

tctctatttc tgggtgaagg gtcttgggtg tgggggtatt gctacggtct ttttaattata 2522

ataaatattt attgaatgct tc 2544

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<211> 712

<212> PRT

<213> Homo sapiens

<400> 154

Met Ala Cys Thr Gly Pro Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly

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Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr

20 25 30

Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu

35 40 45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu

50 55 60

566/735

Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val

65 70 75 80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val

85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser

100 105 110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg

115 120 125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys

130 135 140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser

145 150 155 160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg

165 170 175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys

180 185 190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu

195 200 205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro

567/735

210 215 220

His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro
225 230 235 240

Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
 245 250 255

Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro
 260 265 270

Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro
 275 280 285

Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys
 290 295 300

Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu
305 310 315 320

Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu
 325 330 335

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
 340 345 350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Ser
 355 360 365

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
370 375 380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
385 390 395 400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
405 410 415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
420 425 430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
435 440 445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
450 455 460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
465 470 475 480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
485 490 495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
500 505 510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
515 520 525

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Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln

530

535

540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg

545

550

555

560

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser

565

570

575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly

580

585

590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro

595

600

605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp

610

615

620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr

625

630

635

640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro

645

650

655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln

660

665

670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln

570/735

675 680 685

Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala Pro

690 695 700

Glu Asp Lys Thr Gln Glu Ala Glu

705 710

<210> 155

<211> 3456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (281).. (3016)

<400> 155

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ggaggagagc tctgtggatg gcaaagggga ccggaagagc acaggcctga aactctccaa 180

gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt 240

tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca 295

571/735

Met Lys Lys Lys Ser

1

5

ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg 343

Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu

10

15

20

ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc 391

Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu

25

30

35

acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc 439

Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala

40

45

50

cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac 487

Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp

55

60

65

tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc 535

Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro

70

75

80

85

ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac 583

Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp

90

95

100

atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg 631

Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly

572/735

105	110	115	
gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct 679			
Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser			
120	125	130	
ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag 727			
Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys			
135	140	145	
aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc 775			
Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser			
150	155	160	165
acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc 823			
Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly			
170	175	180	
aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg 871			
Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly			
185	190	195	
ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag 919			
Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu			
200	205	210	
gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc 967			
Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu			
215	220	225	

att gat ggg cat gag aag ctg acc cgg cgg cag tgc cac cag cag gag 1015

Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu

230

235

240

245

gcg gtg tgg gag ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg 1063

Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu

250

255

260

cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag 1111

Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu

265

270

275

tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc 1159

Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile

280

285

290

ccg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg 1207

Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala

295

300

305

ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg 1255

Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly

310

315

320

325

gac ttc ctc aaa ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac 1303

Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr

330

335

340

atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc 1351
Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly

345

350

355

ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag 1399
Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu

360

365

370

aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa 1447
Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys

375

380

385

ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg 1495
Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu

390

395

400

405

agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc 1543
Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile

410

415

420

ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag 1591
Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln

425

430

435

cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc 1639
Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala

440

445

450

tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag 1687

575/735

Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys
 455 460 465

gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg 1735
 Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro
 470 475 480 485

gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag 1783
 Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu
 490 495 500

ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg 1831
 Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu
 505 510 515

ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc 1879
 Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile
 520 525 530

agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac 1927
 Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp
 535 540 545

cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta 1975
 Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val
 550 555 560 565

ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg 2023
 Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp
 576/735

570	575	580	
gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca 2071			
Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala			
585	590	595	
cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag 2119			
Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu			
600	605	610	
gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa 2167			
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu			
615	620	625	
ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg 2215			
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg			
630	635	640	645
aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc 2263			
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser			
650	655	660	
acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc 2311			
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser			
665	670	675	
tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc 2359			
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr			
680	685	690	

tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg 2407
 Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu
 695 700 705

ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac 2455
 Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr
 710 715 720 725

ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca 2503
 Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro
 730 735 740

atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc 2551
 Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser
 745 750 755

cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg 2599
 Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu
 760 765 770

agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc 2647
 Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu
 775 780 785

cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc 2695
 Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser
 790 795 800 805

cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg 2743

Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg

810

815

820

act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg 2791

Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly

825

830

835

gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg 2839

Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly

840

845

850

gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg 2887

Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly

855

860

865

gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag 2935

Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln

870

875

880

885

cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg 2983

His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu

890

895

900

ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gaggcccca 3036

Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val

905

910

agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc 3096

579/735

ttcagctact gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc 3156

gggcccogatt tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtacca 3216

ccccacctgc ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag 3276

tcttcagggc tgggctccta ggctgcccatt cctacttcta ccctcactgg cctccagtgg 3336

gattcactcc tgcctgccc ccaccttccc agtcccacag gccaccctg gcttgggctg 3396

ggttctgtga agttacgtat ttattgagct ttgggttctt ttataaagac ttgtctagac 3456

<210> 156

<211> 912

<212> PRT

<213> Homo sapiens

<400> 156

Met Lys Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg

1 5 10 15

Lys Gly Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn

20 25 30

Thr Pro Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr

35 40 45

Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu
50 55 60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro
65 70 75 80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg
85 90 95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met
100 105 110

Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr
115 120 125

Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr
130 135 140

Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe
145 150 155 160

Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met
165 170 175

Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro
180 185 190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu
195 200 205

Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp

210

215

220

Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln

225

230

235

240

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser

245

250

255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu

260

265

270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg

275

280

285

Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp

290

295

300

Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala

305

310

315

320

Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser

325

330

335

Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met

340

345

350

Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr

582/735

Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser
355 360 365
370 375 380

Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu
385 390 395 400

Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala
405 410 415

Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn
420 425 430

Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val
435 440 445

Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val
450 455 460

Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile
465 470 475 480

Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser
485 490 495

Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe
500 505 510

Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu
515 520 525

Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys
530 535 540

Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu
545 550 555 560

Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala
565 570 575

Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu
580 585 590

Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln
595 600 605

Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu
610 615 620

Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser
625 630 635 640

Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys
645 650 655

Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro
660 665 670
584/735

Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser

675

680

685

Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro

690

695

700

Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser

705

710

715

720

Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe

725

730

735

Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser

740

745

750

Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr

755

760

765

Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser

770

775

780

Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr

785

790

795

800

Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro

805

810

815

Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser

585/735

820	825	830
Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val		
835	840	845
Gly Cys Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly		
850	855	860
Asp Leu Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro		
865	870	875
		880
Gly Val Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg		
885	890	895
Ile Arg Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val		
900	905	910

<210> 157

<211> 3609

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (152).. (3169)

<400> 157

586/735

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ggatgtatgt caccacgccg actgccagca gctgcaccgc cggggggccc tcaacctctg 120

cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc 172
Met His Tyr Asp Gly His Val
1 5

cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc 220
Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser
10 15 20

acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag 268
Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu
25 30 35

gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca 316
Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr
40 45 50 55

ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac 364
Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp
60 65 70

cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att 412
Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile
75 80 85

gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg 460
587/735

Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val
90 95 100

ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac 508
Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp
105 110 115

atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc 556
Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala
120 125 130 135

tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct 604
Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro
140 145 150

gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg 652
Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu
155 160 165

agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc gcc ctg gag 700
Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu
170 175 180

cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct 748
Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro
185 190 195

ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg gag gcg agc atc 796
Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile
588/735

200	205	210	215	
ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc				844
Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly				
	220	225	230	
agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc				892
Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala				
	235	240	245	
agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt				940
Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe				
	250	255	260	
ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc				988
Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr				
	265	270	275	
tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac				1036
Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp				
	280	285	290	295
cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat				1084
His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn				
	300	305	310	
gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat				1132
Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His				
	315	320	325	
		589/735		

gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag 1180

Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu

330

335

340

ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc 1228

Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile

345

350

355

aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg 1276

Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu

360

365

370

375

tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg 1324

Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala

380

385

390

cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag 1372

Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu

395

400

405

aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa 1420

Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys

410

415

420

ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac atc cgc tac tgc 1468

Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys

425

430

435

atg gag gag gag ggc tgc atg gag tac atg cgc ggc ctg ctg cgc gac 1516

Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp

440 445 450 455

aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag aag cac cca cag 1564

Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln

460 465 470

tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg 1612

Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg

475 480 485

ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg agg aag acc gag 1660

Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu

490 495 500

gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc ggc tcc gtg gag 1708

Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu

505 510 515

cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg 1756

Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg

520 525 530 535

cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg 1804

Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val

540 545 550

gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac 1852

591/735

Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys Glu Phe Leu His
555 560 565

ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg gag gag acg cgg 1900
Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg
570 575 580

cag ctg ctg ctg gag ggg agc ctg agg atg aag gag ggg aag gac agc 1948
Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser
585 590 595

aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg ctg ttg gtg acc 1996
Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr
600 605 610 615

aaa gca gtg aag aag gca gag agg acc agg gtc atc agg cca ccc ctg 2044
Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu
620 625 630

ctc gtg gac aag att gtg tgc cgg gag cta cgg gac cct ggg tcc ttc 2092
Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp Pro Gly Ser Phe
635 640 645

ctc ctt atc tac ctg aat gag ttt cac agt gct gta ggg gcc tac acg 2140
Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val Gly Ala Tyr Thr
650 655 660

ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg gtg gac acc att 2188
Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile
592/735

665	670	675	
tac aat gcc cag aac cag ctg caa cag ctg cgt gca cag gag ccc cca 2236			
Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala Gln Glu Pro Pro			
680	685	690	695
ggc agt cag cag ccc ctg cag agc ctg gaa gag gag gag gat gag cag 2284			
Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln			
	700	705	710
gag gag gaa gag gag gag gag gag gag gag gaa ggc gag gac agt 2332			
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Glu Asp Ser			
	715	720	725
ggc act tca gct gcc agc tcc cct acc atc atg cgg aaa agc agc ggc 2380			
Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg Lys Ser Ser Gly			
	730	735	740
agc ccc gac tct cag cac tgt gcc tca gat ggc tcc acg gag acc ctg 2428			
Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser Thr Glu Thr Leu			
	745	750	755
gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc tcc ccc gag ttc 2476			
Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser Ser Pro Glu Phe			
760	765	770	775
gac agc ggt cct ttc agc tcc cag tct gat gag acc tct ctc agc acc 2524			
Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr Ser Leu Ser Thr			
	780	785	790
593/735			

act gcc tca tct gcc acg ccc acc agt gag ctg ctg ccc ctg ggt ccg 2572

Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro

795

800

805

gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc 2620

Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser

810

815

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cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta 2668

Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu

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gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc cct cca ccc tcg 2716

Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser

840

845

850

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ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc 2764

Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro

860

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cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca 2812

His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala

875

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ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc cgc agc ctg tca 2860

Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser

890

895

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gag ctc tgc ctg gct gtt cca gcc cca ggt att agg act cag ggc tcc 2908

Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser

905

910

915

cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct 2956

Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro

920

925

930

935

ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg gaa cct gca ggc 3004

Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly Glu Pro Ala Gly

940

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950

tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg gcc tct ccc agg 3052

Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly Ala Ser Pro Arg

955

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gtc cag cct gag ccc cca cca ggg gtc tct gcc cag cac agg aag ctg 3100

Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu

970

975

980

acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc 3148

Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser

985

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acg ctc act gcc tcg gag gtc tgagcagagg gaggcccca agagtgccat 3199

Thr Leu Thr Ala Ser Glu Val

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595/735

gcctcctgta tgcattgagcc ggatgctggg caggatccct gcctacgccc gggcccgatt 3319

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ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag tcttcagggc 3439

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tgccttcccc ccaccttccc agtcccacag gccaccctg gcttgggctg gggtctgtga 3559

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Pro Ala Val Asp Leu Glu Glu Glu Glu Glu Ser Ser Val Asp Gly

35 40 45

Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala
50 55 60

Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys
65 70 75 80

Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys
85 90 95

Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly
100 105 110

Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro
115 120 125

Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg
130 135 140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly
145 150 155 160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly
165 170 175

Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu
180 185 190

Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu
195 200 205

Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser

210

215

220

Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp

225

230

235

240

Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser

245

250

255

Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln

260

265

270

Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu

275

280

285

Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp

290

295

300

Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp

305

310

315

320

Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His

325

330

335

Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile

340

345

350

Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn

598/735

355 360 365
Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe
370 375 380
Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser
385 390 395 400
Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu
405 410 415
Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe
420 425 430
Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr
435 440 445
Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr
450 455 460
Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met
465 470 475 480
Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys
485 490 495
Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val
500 505 510

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys

515

520

525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg

530

535

540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys

545

550

555

560

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly

565

570

575

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg

580

585

590

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe

595

600

605

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr

610

615

620

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu

625

630

635

640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His

645

650

655

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys

660

665

670

600/735

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys

515

520

525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg

530

535

540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys

545

550

555

560

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly

565

570

575

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg

580

585

590

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe

595

600

605

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr

610

615

620

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu

625

630

635

640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His

645

650

655

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys

660

665

670

600/735

Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln

675

680

685

Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu

690

695

700

Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu

705

710

715

720

Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr

725

730

735

Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser

740

745

750

Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp

755

760

765

Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser

770

775

780

Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser

785

790

795

800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp

805

810

815

Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala

601/735

820 825 830
Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg
835 840 845
Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val
850 855 860
Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala
865 870 875 880
Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser
885 890 895
Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro
900 905 910
Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp
915 920 925
Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys
930 935 940
Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu
945 950 955 960
Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val
965 970 975

Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg

980

985

990

Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val

995

1000

1005

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cactggcgcg atgcgggccc tcctctcggc tg atg ggt tgg aag ccc agc gag 113

Met Gly Trp Lys Pro Ser Glu

1

5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

10

15

20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga 209

603/735

Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
 25 30 35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257
 Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
 40 45 50 55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac 305
 Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
 60 65 70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc 353
 Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
 75 80 85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc 401
 Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
 90 95 100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg 449
 Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
 105 110 115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497
 Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
 120 125 130 135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545
 Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
 604/735

140	145	150	
gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593			
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys			
155	160	165	
cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641			
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg			
170	175	180	
cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg 689			
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg			
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ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg 737			
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp			
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ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc 785			
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile			
220	225	230	
cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg 833			
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp			
235	240	245	
gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg 881			
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val			
250	255	260	
605/735			

gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac 929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp
265 270 275

cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt 977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser
280 285 290 295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg 1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu
300 305 310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac 1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn
315 320 325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc 1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile
330 335 340

acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg 1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp
345 350 355

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc 1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
360 365 370 375

gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag 1265

Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln

380

385

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gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc 1313

Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg

395

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gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca 1361

Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala

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gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac 1409

Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr

425

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cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag 1457

Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu

440

445

450

455

aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag 1505

Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys

460

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470

agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt 1553

Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly

475

480

485

aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg 1601

607/735

Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val

490

495

500

gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg 1649

Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu

505

510

515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg 1697

Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val

520

525

530

535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg 1745

Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu

540

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ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg 1793

Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg

555

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gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg 1841

Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val

570

575

580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt 1889

Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys

585

590

595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc 1937

Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala

608/735

600 605 610 615

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Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu

 620 625 630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg 2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu

 635 640 645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att 2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile

 650 655 660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc 2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe

 665 670 675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag 2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln

680 685 690 695

atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag 2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys

 700 705 710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg 2273
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu

 715 720 725

609/735

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu
730 735 740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu
745 750 755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu
760 765 770 775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg 2465
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr
780 785 790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val
795 800 805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag 2561
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu
810 815 820

ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag 2609
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu
825 830 835

cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
840 845 850 855

acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc 2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
860 865 870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg 2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
875 880 885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg 2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
890 895 900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
905 910 915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
940 945 950

cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc 2993
611/735

Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe

955

960

965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041

Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala

970

975

980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089

Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val

985

990

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aaaagaaaga ttctcgat

3168

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Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr

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30

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp

612/735

35 40 45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
50 55 60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
65 70 75 80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
85 90 95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
100 105 110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
130 135 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
145 150 155 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
165 170 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
180 185 190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val

195

200

205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys

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215

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Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg

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230

235

240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg

245

250

255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala

260

265

270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala

275

280

285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly

290

295

300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln

305

310

315

320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln

325

330

335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln

340

345

350

614/735

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys

355

360

365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu

370

375

380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp

385

390

395

400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly

405

410

415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser

420

425

430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp

435

440

445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu

450

455

460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu

465

470

475

480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu

485

490

495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala

615/735

500 505 510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
515 520 525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
530 535 540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545 550 555 560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
565 570 575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
580 585 590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
595 600 605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
610 615 620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625 630 635 640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
645 650 655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp

660

665

670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn

675

680

685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp

690

695

700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val

705

710

715

720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys

725

730

735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala

740

745

750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly

755

760

765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu

770

775

780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu

785

790

795

800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser

805

810

815

617/735

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly

820

825

830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro

835

840

845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His

850

855

860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser

865

870

875

880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val

885

890

895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val

900

905

910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala

915

920

925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser

930

935

940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp

945

950

955

960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro

618/735

965

970

975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg

980

985

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Asp Arg Ile Gln Ile Phe Val

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Met Gly Trp Lys Pro Ser Glu

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gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

10

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619/735

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga 209
 Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
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gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257
 Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
 40 45 50 55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac 305
 Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
 60 65 70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc 353
 Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
 75 80 85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc 401
 Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
 90 95 100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg 449
 Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
 105 110 115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497
 Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
 120 125 130 135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545

Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg

140

145

150

gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593

Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys

155

160

165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641

His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg

170

175

180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg 689

Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg

185

190

195

ggc atc ttc cag gga ggc aag gtg gtg cga ggc ccc ttc tgg gag tgg 737

Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp

200

205

210

215

ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc 785

Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile

220

225

230

cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg 833

Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp

235

240

245

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg 881

621/735

Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val
 250 255 260

gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac 929
 Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp
 265 270 275

cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt 977
 His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser
 280 285 290 295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg 1025
 Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu
 300 305 310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac 1073
 Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn
 315 320 325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc 1121
 Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile
 330 335 340

acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg 1169
 Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp
 345 350 355

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc 1217
 Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
 622/735

360 365 370 375

gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag 1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln

380 385 390

gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc 1313
Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg

395 400 405

gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca 1361
Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala

410 415 420

gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac 1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr

425 430 435

cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag 1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu

440 445 450 455

aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag 1505
Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys

460 465 470

agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt 1553
Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly

475 480 485

623/735

aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg 1601
 Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val
 490 495 500

gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg 1649
 Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu
 505 510 515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg 1697
 Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val
 520 525 530 535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg 1745
 Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu
 540 545 550

ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg 1793
 Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg
 555 560 565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg 1841
 Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val
 570 575 580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt 1889
 Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys
 585 590 595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc 1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
600 605 610 615

atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag 1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
620 625 630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg 2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
635 640 645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att 2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
650 655 660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc 2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
665 670 675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag 2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
680 685 690 695

atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag 2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
700 705 710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg 2273
625/735

Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu

715

720

725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321

Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu

730

735

740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369

Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu

745

750

755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417

Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu

760

765

770

775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg 2465

Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr

780

785

790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513

Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val

795

800

805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag 2561

Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu

810

815

820

ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag 2609

Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu

626/735

825 830 835

cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly

840 845 850 855

acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc 2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro

860 865 870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg 2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu

875 880 885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg 2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg

890 895 900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg

905 910 915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro

920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu

940 945 950

627/735

cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc 2993
Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe
955 960 965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
970 975 980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg 3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
985 990 995

tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg cccccgccct gtgttttata 3149

aaaagaaaga ttctcgat 3168

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<213> Homo sapiens

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Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln
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Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr
20 25 30
628/735

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp

35

40

45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp

50

55

60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val

65

70

75

80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val

85

90

95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr

100

105

110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val

115

120

125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg

130

135

140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr

145

150

155

160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg

165

170

175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly

629/735

180	185	190
Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val		
195	200	205
Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys		
210	215	220
Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg		
225	230	235
		240
Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg		
	245	250
		255
Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala		
260	265	270
Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala		
275	280	285
Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly		
290	295	300
Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln		
305	310	315
		320
Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln		
	325	330
		335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln

340

345

350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys

355

360

365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu

370

375

380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp

385

390

395

400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly

405

410

415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser

420

425

430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp

435

440

445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu

450

455

460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu

465

470

475

480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu

485

490

495

631/735

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala

500

505

510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu

515

520

525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr

530

535

540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val

545

550

555

560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser

565

570

575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg

580

585

590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser

595

600

605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly

610

615

620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr

625

630

635

640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His

632/735

645 650 655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
660 665 670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
675 680 685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
690 695 700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705 710 715 720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
725 730 735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
740 745 750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
755 760 765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
770 775 780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
785 790 795 800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser

805

810

815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly

820

825

830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro

835

840

845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His

850

855

860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser

865

870

875

880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val

885

890

895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val

900

905

910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala

915

920

925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser

930

935

940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp

945

950

955

960

634/735

Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro

965

970

975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg

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Asp Arg Ile Gln Ile Phe Val

995

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<222> (91).. (2649)

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Met Ile Ala Trp Arg Leu Pro Leu

1

5

tgc gtg etc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg 162

635/735

Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly

10 15 20

ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg 210

Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala

25 30 35 40

gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc 258

Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr

45 50 55

gtg acc cgc aac cgg acc gag ggt gtg cga gtg tct gtg aat gtc ctg 306

Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu

60 65 70

aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag 354

Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu

75 80 85

gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag 402

Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln

90 95 100

cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc 450

Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro

105 110 115 120

acc aag aat gag tct gag atc cag ttt ttc tat gtg gac gtg tct acc 498

Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr

636/735

125	130	135	
ctg tca ccc gtc aat acc act tac cag ctc cga gtc aac cgt gtg gac			546
Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp			
140	145	150	
aat ttt gtg ctc agg act gga gag ctg ttt acc ttt aat acc act gca			594
Asn Phe Val Leu Arg Thr Gly Glu Leu Phe Thr Phe Asn Thr Thr Ala			
155	160	165	
gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg			642
Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser			
170	175	180	
gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc			690
Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile			
185	190	195	200
tcc atc cag gat gtc ctg tgc cct gtc tat gat ctg gac aac agt gta			738
Ser Ile Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Ser Val			
205	210	215	
gcc ttc att ggc atg tac cag acg atg act aag aag gca gcc atc act			786
Ala Phe Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr			
220	225	230	
gtg cag cgg aaa gac ttc ccc agc aac agc ttc tat gtg gtg gtg gta			834
Val Gln Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val			
235	240	245	

gtg aag act gag gac cag gcc tgc gga ggg tcc ttg ccc ttc tac cct 882
 Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro
 250 255 260

ttt gtg gaa gat gag cca gtg gat caa ggg cac cgt cag aaa aca ctg 930
 Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu
 265 270 275 280

tca gtg ctg gtc tct cag gct gtc aca tct gag gcc tat gtt ggt ggg 978
 Ser Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Gly Gly
 285 290 295

atg ctc ttt tgc ctg ggc ata ttc ttg tcc ttc tac ctg ctg act gtg 1026
 Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val
 300 305 310

ctg ctg gcc tgt tgg gag aac tgg agg caa agg aag aag acc ttg ctg 1074
 Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu
 315 320 325

gtg gcc ata gac cga gcc tgc cca gaa agt ggt cac gct cgg gtc ttg 1122
 Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu
 330 335 340

gct gat tca ttt cct ggc agt gcc cct tac gag ggt tac aac tat ggc 1170
 Ala Asp Ser Phe Pro Gly Ser Ala Pro Tyr Glu Gly Tyr Asn Tyr Gly
 345 350 355 360

tcc ttt gaa aat ggt tcc gga tcc act gac ggg ttg gtt gaa agc gca 1218

Ser Phe Glu Asn Gly Ser Gly Ser Thr Asp Gly Leu Val Glu Ser Ala

365

370

375

ggt tca ggg gac ctc tcc tac agt tac cag ggg cac gac cag ttc aag 1266

Gly Ser Gly Asp Leu Ser Tyr Ser Tyr Gln Gly His Asp Gln Phe Lys

380

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cgg cgc ctt ccc tct ggc cag atg cgg cag ctg tgc att gcc atg gac 1314

Arg Arg Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Asp

395

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cgc tcc ttt gac gca gtg ggt cct cgg cct cga ctg gac tcc atg agc 1362

Arg Ser Phe Asp Ala Val Gly Pro Arg Pro Arg Leu Asp Ser Met Ser

410

415

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tcc gtg gaa gag gat gac tac gac acg ctg act gac atc gac tca gac 1410

Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp

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aaa aac gtc att cga acc aag caa tac ctc tgt gtg gct gat ctg gca 1458

Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala

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Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp

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aac ata gcc acc att gcg gtc ttc tac gca ctt cct gtg gtg cag ctg 1554

639/735

Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu

475

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Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile

490

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Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala

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Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu

525

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ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg 1746

Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu

540

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ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt 1794

Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe

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ggt ctg ttt tac gcc atg ggc aca gca ctg atg atg gag ggg cta ctt 1842

Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu

570

575

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Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp

640/735

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Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr			
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Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala			
620	625	630	
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Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly			
635	640	645	
aaa ggg aac acg gcc ttc tgg att gtc ttc tcc gtc att cac atc atc 2082			
Lys Gly Asn Thr Ala Phe Trp Ile Val Phe Ser Val Ile His Ile Ile			
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Ser Thr Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys			
665	670	675	680
ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac 2178			
Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp			
685	690	695	
tgc atc cgg cag tgc agc ggg ccc ctt tac acg gac cgc atg gtg ctt 2226			
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu			
700	705	710	
641/735			

ctg gtc atg ggc aac att atc aac tgg tgc ctg gct gca tac gga ctc 2274
 Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu
 715 720 725

atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc 2322
 Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile
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 Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg
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agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc 2418
 Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr
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 Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser
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Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val

35 40 45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly

50 55 60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu

65 70 75 80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro

85 90 95

Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val

100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln

115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr

130 135 140

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Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu
145 150 155 160

Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
165 170 175

Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
195 200 205

Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
245 250 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp
260 265 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
275 280 285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe
646/735

290 295 300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305 310 315 320

Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
 325 330 335

Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala
 340 345 350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser
 355 360 365

Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser
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Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
385 390 395 400

Arg Gln Leu Cys Ile Ala Met Asp Arg Ser Phe Asp Ala Val Gly Pro
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Arg Pro Arg Leu Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
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Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
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Tyr Leu Cys Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg

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455

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Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe

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470

475

480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val

485

490

495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala

500

505

510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu

515

520

525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg

530

535

540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu

545

550

555

560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr

565

570

575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro

580

585

590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala

595

600

605

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Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
610 615 620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625 630 635 640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
645 650 655

Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln
660 665 670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg
675 680 685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
690 695 700

Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn
705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
649/735

755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu

770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu

785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp

805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe

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Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp

835 840 845

Lys Ile Tyr Val Phe

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650/735

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Met Phe Ala Leu Gly Leu Pro Phe Leu Val

1 5 10

ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag 161

Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys

15 20 25

aac gtc tcg cag aaa gac gcc gag ttt gag cgc acc tac gtg gac gag 209

Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu

30 35 40

gtc aac agc gag ctg gtc aac atc tac acc ttc aac cat act gtg acc 257

Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr

45 50 55

cgc aac agg aca gag ggc gtg cgt gtg tct gtg aac gtc ctg aac aag 305

Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys

60 65 70

cag aag ggg gcg ccg ttg ctg ttt gtg gtc cgc cag aag gag gct gtg 353

Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val

75 80 85 90

gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag 401

Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys

95

100

105

tac ctc tac caa aaa gtg gaa cga acc ctg tgt cag ccc ccc acc aag 449

Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys

110

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aat gag tcg gag att cag ttc ttc tac gtg gat gtg tcc acc ctg tca 497

Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser

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cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt 545

Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe

140

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gtg ctc agg act ggg gag cag ttc agc ttc aat acc aca gca gca cag 593

Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln

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170

ccc cag tac ttc aag tat gag ttc cct gaa ggc gtg gac tcg gta att 641

Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile

175

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Val Lys Val Thr Ser Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile

190

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200

cag gat gtg ctg tgt cct gtc tat gac ctg gac aac aac gta gcc ttc 737

652/735

Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe

205

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215

atc ggc atg tac cag acg atg acc aag aag gcg gcc atc acc gta cag 785

Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln

220

225

230

cgc aaa gac ttc ccc agc aac agc ttt tat gtg gtg gtg gtg gtg aag 833

Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys

235

240

245

250

acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca 881

Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala

255

260

265

gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg 929

Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val

270

275

280

ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc 977

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285

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295

ttt tgc ctg ggt ata ttt ctc tcc ttt tac ctg ctg acc gtc ctc ctg 1025

Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu

300

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310

gcc tgc tgg gag aac tgg agg cag aag aag aag acc ctg ctg gtg gcc 1073

Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

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315 320 325 330

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Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp

 335 340 345

tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt 1169
Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe

 350 355 360

gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act 1217
Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr

 365 370 375

ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc 1265
Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg

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ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc 1313
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser

395 400 405 410

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Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val

 415 420 425

gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat 1409
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn

 430 435 440

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Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys
445 450 455

gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att 1505
Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile
460 465 470

gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc 1553
Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile
475 480 485 490

acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac 1601
Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr
495 500 505

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Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn
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aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg 1697
Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu
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aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt 1793

Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu

555 560 565 570

ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct 1841

Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala

575 580 585

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Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser

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Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys

605 610 615

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Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu

620 625 630

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Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly

635 640 645 650

aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc 2081

Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr

655 660 665

ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac 2129

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Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp

670

675

680

tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc 2177

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685

690

695

cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc 2225

Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val

700

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atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg 2273

Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met

715

720

725

730

cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac 2321

Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn

735

740

745

ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg 2369

Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly

750

755

760

gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg 2417

Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val

765

770

775

gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg 2465

Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp

657/735

780 785 790

cag aaa acc cct gca gag tcg agg gag cac aac cgg gac tgc atc ctc 2513
Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu

795 800 805 810

ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc 2561
Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile

815 820 825

gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg 2609
Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly

830 835 840

tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg 2658
Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly

845 850 855

tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca 2718

ggaagggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggaccaggg 2778

ctggcttcta agtttccgtc cagtcttcag gcaagttctg tgtagtcat gcacacacat 2838

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gttccttga tccccttcgt ccacactggt ccaccccaga tgctgaggat gggggagctc 2958

aggcggggcc tctgctttgg ggatgggaat gtgtttttct cccaaacttg tttttatagc 3018

658/735

tctgcttgaa gggctgggag atgaggtggg tctggatctt ttctcagagc gtctccatgc 3078

tatggttgca tttccgtttt ctatgaatga atttgattc aataaacaac cagactcagt 3138

<210> 166

<211> 855

<212> PRT

<213> Homo sapiens

<400> 166

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Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln Lys Asp

20 25 30

Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val

35 40 45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly

50 55 60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu

65 70 75 80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro

85 90 95

659/735

Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val

100

105

110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln

115

120

125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr

130

135

140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu

145

150

155

160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr

165

170

175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn

180

185

190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro

195

200

205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr

210

215

220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser

225

230

235

240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys

660/735

245 250 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp
260 265 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
275 280 285

Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe
290 295 300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305 310 315 320

Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
325 330 335

Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser
340 345 350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser
355 360 365

Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly
370 375 380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
385 390 395 400

Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr

405

410

415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp

420

425

430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln

435

440

445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg

450

455

460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe

465

470

475

480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val

485

490

495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala

500

505

510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu

515

520

525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg

530

535

540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu

545

550

555

560

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Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr

565

570

575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro

580

585

590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala

595

600

605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn

610

615

620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe

625

630

635

640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile

645

650

655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln

660

665

670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg

675

680

685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro

690

695

700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn

663/735

705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
 725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
 740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
 755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
 770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
 805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
 820 825 830

Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser
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Ser Cys Leu Leu Pro Cys Gly
 850 855

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<222> (56).. (571)

<400> 167

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Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu

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10

15

gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat 154

Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr

20

25

30

cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg 202

Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg

35

40

45

tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc 250

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Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe

50 55 60 65

ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc 298

Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile

70 75 80

cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat 346

Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn

85 90 95

gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag 394

Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln

100 105 110

ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct 442

Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro

115 120 125

gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc 490

Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro

130 135 140 145

cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct 538

Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro

150 155 160

ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591

Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys

666/735

165

170

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gggc 2815

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<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

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669/735

Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu

20

25

30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser

35

40

45

Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp

50

55

60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe

65

70

75

80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe

85

90

95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln

100

105

110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn

115

120

125

Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser

130

135

140

Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr

145

150

155

160

Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys

670/735

165

170

<210> 169

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agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile

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10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219

Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu

15

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25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267

Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala

30

35

40

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acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315

Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn

45 50 55 60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363

Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu

65 70 75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411

Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr

80 85 90

cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459

Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu

95 100 105

cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg 507

Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala

110 115 120

gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555

Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr

125 130 135 140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603

Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn

145 150 155

tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat 651

Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn

160

165

170

cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc 699

Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser

175

180

185

cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt 747

Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser

190

195

200

acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggg cct 795

Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro

205

210

215

220

gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg 843

Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg

225

230

235

gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc 891

Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr

240

245

250

tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag 939

Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu

255

260

265

ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc 987

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Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser

270

275

280

agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc 1035

Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr

285

290

295

300

acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca 1083

Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro

305

310

315

gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc 1131

Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro

320

325

330

cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa 1179

Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys

335

340

345

ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct 1227

Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro

350

355

360

act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac 1275

Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp

365

370

375

380

ggg agc agc aga aat gag gag acc cca gca gct cca aca ccc gcc ggc 1323

Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly

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385	390	395	
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400	405	410	
ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta 1419			
Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val			
415	420	425	
gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc 1467			
Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser			
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Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr			
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aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc 1563			
Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile			
465	470	475	
cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc 1611			
Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly			
480	485	490	
ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc 1659			
Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys			
495	500	505	
675/735			

cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg 1707

His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly

510

515

520

gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac 1755

Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His

525

530

535

540

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tgggttcttt tcaggaacc attgctggac aaggcacagg agccacctcc atttctgagc 2955

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ccgtcagcct ccagggatct acaccctgcc ttggctgcta cagctttttc actccactgc 3075

cctaggggag ttcagcaacc taatgatctc tatctctgaa catctcttca tcccatgctc 3135

caagtccagc aacctgcacc ctggaaccag gagtggaccc taccgggct gtctgtatta 3195

atccccatcc cccaccacca atcttaaaaa gccctctgtc cccctaccct aaaccccagt 3255

taggtacca tgctgggcag gtcagttaac aatttatgca caggtactag ttttattgta 3315

ttaccgttcc agggtagctt tg 3337

<210> 170

<211> 540

<212> PRT

<213> Homo sapiens

<400> 170

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro

20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu

35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg

50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu

65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln

85 90 95

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Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
100 105 110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
115 120 125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130 135 140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145 150 155 160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
165 170 175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
180 185 190

Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala
195 200 205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
210 215 220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225 230 235 240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
679/735

245 250 255
Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
260 265 270
Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
275 280 285
Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
290 295 300
Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
305 310 315 320
Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
325 330 335
Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
340 345 350
Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
355 360 365
Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
370 375 380
Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385 390 395 400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser

405

410

415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe

420

425

430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly

435

440

445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly

450

455

460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu

465

470

475

480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln

485

490

495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser

500

505

510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val

515

520

525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His

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<210> 171

<211> 3579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 171

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gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccg 180

gggaaggagg cagggaagg ccgggcttgg gggcaggtgg tccgggcac cagccttgaa 240

g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1 5 10 15

gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

20 25 30

atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc 385

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35 40 45

682/735

ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc 433

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

50

55

60

aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc 481

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys

65

70

75

80

atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac 529

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp

85

90

95

ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga 577

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly

100

105

110

gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag 625

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys

115

120

125

cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg 673

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu

130

135

140

gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc 721

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser

145

150

155

160

gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg 769

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu

165

170

175

ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg 817

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro

180

185

190

ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc 865

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser

195

200

205

cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc 913

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro

210

215

220

agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca 961

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro

225

230

235

240

ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct 1009

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro

245

250

255

ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc 1057

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu

260

265

270

cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc 1105

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His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg

275

280

285

gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag 1153

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu

290

295

300

ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca 1201

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro

305

310

315

320

gac cca ccg tca cca ccg tgc cag cct ccg acc ccc gct acg gcg ccc 1249

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro

325

330

335

tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg 1297

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu

340

345

350

gag cag cgg atg gag cgg tac cag gtg gcc gca gcc cag gcc aag agc 1345

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser

355

360

365

aag ggg gac cag cgg aaa gct cga atg cac gag cgc atc gtc aag caa 1393

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln

370

375

380

tac caa gat gcc atc cga gcc cac aag gct ggc cga gcc gtg gat gtc 1441

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val

685/735

385 390 395 400

gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag 1489
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
405 410 415

gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc 1537
Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
420 425 430

atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag 1585
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
435 440 445

gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa 1633
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
450 455 460

gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa 1681
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465 470 475 480

gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc 1729
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
485 490 495

cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag 1777
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
500 505 510

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cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag 1825

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys

515

520

525

gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac 1873

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp

530

535

540

atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg 1921

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu

545

550

555

560

gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat 1969

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr

565

570

575

ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac 2017

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn

580

585

590

cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag 2065

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys

595

600

605

ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag 2113

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys

610

615

620

caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa 2161
Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625 630 635 640

agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac 2209
Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
645 650 655

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga 2257
Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
660 665 670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat 2305
Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
675 680 685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac 2353
Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
690 695 700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc 2401
Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705 710 715 720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc 2449
Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
725 730 735

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg 2497
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Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly

740

745

750

aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg 2545

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg

755

760

765

gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg 2593

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu

770

775

780

gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag 2641

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu

785

790

795

800

acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg 2689

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val

805

810

815

ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc 2737

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala

820

825

830

cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc 2785

Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu

835

840

845

agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc 2833

Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala

689/735

850	855	860	
ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac 2881			
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr			
865	870	875	880
cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag 2929			
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln			
	885	890	895
ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag 2977			
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln			
	900	905	910
ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc 3025			
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser			
	915	920	925
agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt 3073			
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser			
	930	935	940
gag ctg cag cgg ctc cgc agg tgaggagccc atggggcggg cagccccag 3124			
Glu Leu Gln Arg Leu Arg Arg			
945	950		
aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca 3184			
gacaatcagc ggacaatcgg ttctggactc acccctcatc cgggccccca gccccgccag 3244			

agcctccgtg gctgcgggtg ttgggaacca tgcctgccag ccagtatgtg cccctcaccc 3304

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ccgccccgga gcagggaggg cggctggggc caagccccga gggcccctgc aagcacttta 3424

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ccagcacatg gaataaaata gccagggcca cactc 3579

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<213> Homo sapiens

<400> 172

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1 5 10 15

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

20 25 30

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35 40 45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

50

55

60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys

65

70

75

80

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp

85

90

95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly

100

105

110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys

115

120

125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu

130

135

140

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser

145

150

155

160

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu

165

170

175

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro

180

185

190

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser

195

200

205

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Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro

210 215 220

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro

225 230 235 240

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro

245 250 255

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu

260 265 270

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg

275 280 285

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu

290 295 300

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro

305 310 315 320

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro

325 330 335

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu

340 345 350

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser

693/735

355 360 365

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
370 375 380

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val
385 390 395 400

Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
405 410 415

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
420 425 430

Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
435 440 445

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
450 455 460

Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465 470 475 480

Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
485 490 495

Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
500 505 510

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys

515

520

525

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp

530

535

540

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu

545

550

555

560

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr

565

570

575

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn

580

585

590

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys

595

600

605

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys

610

615

620

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln

625

630

635

640

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp

645

650

655

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly

660

665

670

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Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr

675 680 685

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn

690 695 700

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg

705 710 715 720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe

725 730 735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly

740 745 750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg

755 760 765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu

770 775 780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu

785 790 795 800

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val

805 810 815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala

696/735

820	825	830
Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu		
835	840	845
Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala		
850	855	860
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr		
865	870	875
		880
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln		
885	890	895
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln		
900	905	910
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser		
915	920	925
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser		
930	935	940
Glu Leu Gln Arg Leu Arg Arg		
945	950	

<211> 2796

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (574)..(1683)

<400> 173

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tagtccttaa caaagggaaa gcgataaatg taaataagct cacattttca gaatgagcgg 180

tttgagtaa ggagctcggg cagcccagag tctgctcttt ttgggctggg ctaacctttc 240

cctgtttttt gttttttgtt ttgtttgtt ttgtttttt atggataaaa atatgcgctt 300

ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca 360

ttctctcatc tagcacactc tttcttgggc actcaattga ggaactctct gatcgtctgc 420

ctccagaaaa ttcatgtatt atccaagtct cagataaatc tggtgccaga gtttggtttg 480

aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaaccctt 540

gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594

Met Gly Asp Arg Arg Phe Ile

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1

5

gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga 642
Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly
10 15 20

aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat 690
Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr
25 30 35

aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata 738
Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile
40 45 50 55

acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga 786
Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg
60 65 70

agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt 834
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu
75 80 85

ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac 882
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His
90 95 100

tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc 930
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu
105 110 115

699/735

acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat 978

Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp

120 125 130 135

cgt ttc cta gcc att gtc tat ccc ttc cga tcg cgt acc atc agg acc 1026

Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr

140 145 150

agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc 1074

Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu

155 160 165

agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat 1122

Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn

170 175 180

gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca 1170

Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr

185 190 195

tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att 1218

Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile

200 205 210 215

cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc 1266

Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu

220 225 230

cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg 1314

Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val

235

240

245

ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta 1362

Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val

250

255

260

cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc 1410

Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala

265

270

275

att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att 1458

Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile

280

285

290

295

acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat 1506

Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr

300

305

310

tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat 1554

Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His

315

320

325

ata agg atg gag tgc ctg ttt aag act gag aca cct ctg acc ccc aaa 1602

Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys

330

335

340

cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat 1650

701/735

Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn

345

350

355

aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703

Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe

360

365

370

caggttcagc tacagtgtct cttatgattt ttttcctatg ctataaatag gagaaacaaa 1763

ttgaagctaa tgatactgag aatagagtaa tgtaccaaata gcagtcagat acatttggtt 1823

gaacactatt gtacatatc tgttttgttc agtaattata ggtcaagtct aattacaaca 1883

acaaaaacag atcagcctct tctgttgagt tgacttttca ttacctaaat gaccagtggc 1943

cttgactttt agtgatgtga ggggtatttt taaacttaaa aaaaaaggca ttccagtaat 2003

tttggttaatt ggggtgggcc tataaatata gaacaaattc agggattatt taaaaacatc 2063

tgtgttacta ctgatatatg ctagtatttt tttccttttt tgaattaata ttgaatttat 2123

tttaaaaaaa gaactatttt tacctaattc taataagaca tactgagaaa gagaaatgtg 2183

ttgaatttta aaatattggc aaattttacc tagattttta aaacctaaat gaagtgtttg 2243

aatgaatatg ggtgggaaat ttggaattta gacaacattt acgcatttat aataaccaca 2303

attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363

gttaatcctg aaaggtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423

ttaacagtgt caatttaaaa aaaaaaaaaac ttttaagcaac actatattat ttcttaagat 2483

tttcatttat cctttatggg ggtggggatt ggcttgtaga aaatatttat tcttcatggt 2543

aaatgttggg gacacattac agccagagag ctacagtatt tgtgcccgagg tcaggagtaa 2603

attgaaaaag taagtgaata gaatagtagc agcaagatat cttagagctt atattagtag 2663

tttttaaggt ggtggttaga tagctgtaat ttgaaatcc atactctctt ctgtacattt 2723

tggagcacat tgtagccaag gcgctgctga atttgtgctc aggtcgggag catattgaaa 2783

aagatgtgta cat 2796

<210> 174

<211> 370

<212> PRT

<213> Mus musculus

<400> 174

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Leu Asn Ser

1 5 10 15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35

40

45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe

50

55

60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn

65

70

75

80

Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile

85

90

95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys

100

105

110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe

115

120

125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe

130

135

140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala

145

150

155

160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe

165

170

175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe

180

185

190

704/735

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile

195

200

205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser

210

215

220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile

225

230

235

240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala

245

250

255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr

260

265

270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe

275

280

285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys

290

295

300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys

305

310

315

320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr

325

330

335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu

705/735

340

345

350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser

355

360

365

Thr Phe

370

<210> 175

<211> 2299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)..(1176)

<400> 175

cctaccggtc catagtgtca gagggtgaa cccctgcagc cagcaggcct cctgaaaaaa 60

aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca 108

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser

1

5

10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act 156

Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr

15

20

25

30

706/735

tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac 204

Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr

35

40

45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt 252

Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe

50

55

60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc 300

Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile

65

70

75

acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt 348

Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe

80

85

90

aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc 396

Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu

95

100

105

110

tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg 444

Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met

115

120

125

ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat 492

Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr

130

135

140

cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg 540

Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val

145

150

155

tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct 588

Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser

160

165

170

ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa 636

Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu

175

180

185

190

ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata 684

Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile

195

200

205

ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct 732

Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser

210

215

220

tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct 780

Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser

225

230

235

caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat 828

Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His

240

245

250

atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc 876

708/735

Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe

255 260 265 270

ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa 924

Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu

275 280 285

aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg 972

Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu

290 295 300

aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt 1020

Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe

305 310 315

cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt 1068

Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe

320 325 330

aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa 1116

Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln

335 340 345 350

gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta 1164

Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu

355 360 365

gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc 1216

Glu Ser Thr Phe

370

ctataatitt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

accaaattcca gtcagataca tttgtttgaa ggtatactgt agagtittta ttgctgtttt 1336

gttcagtaat tataggtcaa atctaattac aacaaccaag atggattgcc aaactcttct 1396

gcttggttg aatttcattg tatcgatta tccaggtggc tagtggcatt tgataatata 1456

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tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat 1576

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aaaattaaca ggatttacac aattataatc accagcagtg tgagtttaaa aaacttcgtt 1816

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gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gccaggtca ggagcaaatt gaaaaaaaa ataaagtaat actaaaaaat 2116

caactataa acccaaaaca ttattataaa cctgaattaa tccttttttg aggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttgagc ctaatatagc 2236

caggagctgc tgaatttgtg cccctggatt ggaaccaaatt aaaaaaaaa aaaaaaaatt 2296

cct 2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser

1 5 10 15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe

50 55 60

711/735

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn

65 70 75 80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile

85 90 95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys

100 105 110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe

115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe

130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala

145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe

165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe

180 185 190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile

195 200 205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser

712/735

210 215 220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225 230 235 240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe
275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305 310 315 320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr
325 330 335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
340 345 350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
355 360 365

Thr Phe

370

<210> 177

<211> 973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (30).. (416)

<400> 177

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Met Ala Arg Gly Ser Leu Arg Arg

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ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc 101

Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser

10

15

20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 149

Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser

25

30

35

40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 197

Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg

714/735

45 50 55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 245
Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro

60 65 70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 293
Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu

75 80 85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 341
Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys

90 95 100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 389
Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu

105 110 115 120

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgccca 436
Gly Cys Pro Ala Val Ala Leu Ile Gln

125

gccggggctc gccactcat cattcattca tccattctag agccagtctc tgcctcccag 496

acgcggcgagg agccaagctc ctccaaccac aaggggggtg gggggcggtg aatcacctcc 556

gaggcctggg tccagggttc aggggaacct tccaaggtgt ctggttgccc tgcctctggc 616

tccagaacag aaaggagacc tcacgtggc tcacacaaaa cagctgacac tgactaagga 676

715/735

actgcagcat ttgcacaggg gaggggggtg ccctccttcc tagaggccct gggggccagg 736

ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actagggggc tggcccacta 856

ggagggctgg ccctaagata cagacccccc caactcccca aagcggggag gagatattta 916

ttttggggag agtttggagg ggaggagaaa tttattaata aaagaatctt taacttt 973

<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly

1 5 10 15

Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly

20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys

35 40 45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys

50 55 60

716/735

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
65 70 75 80

Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
85 90 95

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
100 105 110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
115 120 125

Gln

<210> 179

<211> 3631

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (191).. (3244)

<400> 179

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ggcgctggcg caagatgatg ttgctccata ttttaaaacg gagccaggcc taccacagat 120

ccacctggaa gggaaccgcc ttgttctcac ctgccttgcc gaaggagct ggcctttgga 180

gttcaagtgg atg cgc gat gac agt gag ctc acc acc tac agc agc gaa 229

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu

1

5

10

tat aag tac att att cca tct ttg cag aag ctc gat gct ggg ttt tac 277

Tyr Lys Tyr Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr

15

20

25

cgc tgc gtg gtg cga aac aga atg gga gca ctc ctg caa aga aaa tca 325

Arg Cys Val Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser

30

35

40

45

gaa gtt caa gtc gca tat atg gga agt ttc atg gat acg gac cag agg 373

Glu Val Gln Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg

50

55

60

aaa aca gtt tct caa gga cgt gca gcg att cta aac ctg ctg ccc atc 421

Lys Thr Val Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile

65

70

75

acc agc tac ccc aga cct caa gtg act tgg ttt aga gaa ggg cac aag 469

Thr Ser Tyr Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys

80

85

90

att att cca agc aac aga ata gcc atc aca ttg gag aat cag ctg gtg 517

718/735

Ile Ile Pro Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val

95

100

105

atc ctc gcc acc aca acc agt gat gcc ggg gca tac tac gtg cag gcc 565

Ile Leu Ala Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala

110

115

120

125

gtg aat gag aaa aat gga gaa aac aag aca agc cca ttc att cat ttg 613

Val Asn Glu Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu

130

135

140

agc ata gca aga gat gtt ggc aca cct gaa acc atg gcc cca acc att 661

Ser Ile Ala Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile

145

150

155

gtg gtt ccc ccg ggc aac aga agt gtg gtg gct gga tcc agt gag acc 709

Val Val Pro Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr

160

165

170

acc ttg gaa tgt ata gcc agt gcc agg cct gtg gag gac ctg agt gtg 757

Thr Leu Glu Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val

175

180

185

acc tgg aag agg aat gga gtg aga atc acc agt ggc ctc cac agc ttt 805

Thr Trp Lys Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe

190

195

200

205

gga aga cgc ctc acc atc agc aac ccg acg tcc gcg gac acc ggg cca 853

Gly Arg Arg Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro

719/735

210	215	220	
tac gtc tgc gag gcg gcg ctg ccg ggg agc gct ttt gaa ccg gcc agg			901
Tyr Val Cys Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg			
225	230	235	
gcg acg gcc ttt ctt ttc atc ata gag cca cca tat ttt act gct gag			949
Ala Thr Ala Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu			
240	245	250	
ccc gag agt cgg att tca gct gaa gta gaa gaa act gtg gac atc gga			997
Pro Glu Ser Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly			
255	260	265	
tgt caa gcc atg ggg gtc ccc ctt ccc acc ctc cag tgg tac aag gat			1045
Cys Gln Ala Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp			
270	275	280	285
gcc atc tcc atc agc agg ctc cag aat cct cga tac aaa gtg ctc gcc			1093
Ala Ile Ser Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala			
290	295	300	
agc gga ggc ctg cgc atc cag aag ctg cgt cca gag gac tcc gga atc			1141
Ser Gly Gly Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile			
305	310	315	
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Phe Gln Cys Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr			
320	325	330	

tac ctg gat gta acc aat atc gct cca gtg ttc acc cag cgg cca gtg 1237

Tyr Leu Asp Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val

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gac acc aca gtt act gac ggg atg aca gcc att cta agg tgt gag gtg 1285

Asp Thr Thr Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val

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360

365

tcc ggg gct ccc aaa ccc gcc atc acc tgg aaa aga gaa aac cac att 1333

Ser Gly Ala Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile

370

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380

ctg gcc agt ggc tct gtc cgg att cct agg ttc atg ctt ctt gaa tcg 1381

Leu Ala Ser Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser

385

390

395

ggg ggt cta cag atc gcg ccc gtc ttc atc cag gat gcc ggc aac tac 1429

Gly Gly Leu Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr

400

405

410

acc tgc tat gcg gcc aac aca gag ggc tcc ctg aat gca tcg gcc acg 1477

Thr Cys Tyr Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr

415

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ctc act gtg tgg aat cgg acg tcc atc gtc cac cct cct gag gac cac 1525

Leu Thr Val Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His

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445

gtg gtg att aag ggg acc acg gcc acg ctg cac tgt ggt gcc aca cat 1573

Val Val Ile Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His

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gac ccc cgg gtt tca ctc cgc tac gtt tgg aag aag gac aac gtg gcc 1621

Asp Pro Arg Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala

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ctg act cca tcg agc acg tct agg atc gtg gtg gag aag gac ggg tcc 1669

Leu Thr Pro Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser

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495

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Glu Ile Val Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu

510

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gtg att gaa ctg cct cat tca cct cag aac ctc ctg gtc agc cct aat 1813

Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn

530

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540

tct tcc cac agc cac gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat 1861

Ser Ser His Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp

545

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555

gga aac agt cct att ctt tat tac atc gtg gag ctg tct gaa aac aac 1909

722/735

Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn

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565

570

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Ser Pro Trp Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly

575

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585

gtc acc gtg agt ggc ctg act ccg gct cgt acc tat caa ttc cgg gtg 2005

Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val

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605

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ccc cca gaa aca gag cac aac ggg gtg ttg cgt gga tac atc ctc agg 2197

Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg

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cag tat gag ata cag gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc 2341
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ttc agc agg gca gtg acc gag tac acc ttg cag gga gtg ccc acc gcg 2389
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 785 790 795

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Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr
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880 885 890

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Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala
895 900 905

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gga gtg ccc cca gac ctt cct ggt gcc cca tcc aac ctg gtc att tcc 3013
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945 950 955

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caa ggt gtt gga tta cct gcc gag gtc aca cag cca agc cat gaa gcc 3157
Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala
975 980 985

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726/735

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tttgtaatct tactgggagg gctaaagcgt cttctatcat atcgaattgg gacaatgata 3434

gaagacaatc tttgttttgt cactctaaag aaattattgt aagattttat catcaggtat 3494

gacatttaca ccattgatgt aggcttttta aaaaatatat ccagcctgta ttgggttaag 3554

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<212> PRT

<213> Homo sapiens

<400> 180

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35 40 45

Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg Lys Thr Val

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Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile Thr Ser Tyr

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70

75

80

Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys Ile Ile Pro

85

90

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Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val Ile Leu Ala

100

105

110

Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala Val Asn Glu

115

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125

Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu Ser Ile Ala

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Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile Val Val Pro

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155

160

Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr Thr Leu Glu

165

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175

Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val Thr Trp Lys

180

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190

Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe Gly Arg Arg

195

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Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro Tyr Val Cys

210 215 220

Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg Ala Thr Ala

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Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu Pro Glu Ser

245 250 255

Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly Cys Gln Ala

260 265 270

Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp Ala Ile Ser

275 280 285

Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala Ser Gly Gly

290 295 300

Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile Phe Gln Cys

305 310 315 320

Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr Tyr Leu Asp

325 330 335

Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val Asp Thr Thr

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Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val Ser Gly Ala

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355 360 365

Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile Leu Ala Ser
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Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser Gly Gly Leu
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Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr Thr Cys Tyr
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Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr Leu Thr Val
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Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala Leu Thr Pro
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Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser Leu Leu Ile
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515

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Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His

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540

Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser

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555

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Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp

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Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val

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Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val

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Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met

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615

620

Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser

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635

640

Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu

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655

Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu

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665

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Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu

675

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Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu

690

695

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Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg

705

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720

Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln

725

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735

Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp

740

745

750

Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys

755

760

765

Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr

770

775

780

Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu

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790

795

800

Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro

805

810

815

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820 825 830
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835 840 845
Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile
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885 890 895
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900 905 910
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945 950 955 960
Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val
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Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu

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985

990

Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys

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Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<212> DNA

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<223> Description of Artificial Sequence:Primer

<400> 182

cgacctgcag ctcgagcaca

20

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP01/11389

A. CLASSIFICATION OF SUBJECT MATTER (See extra sheet.)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
(See extra sheet.)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Genebank/EMBL/EMBL/DBJ/GeneSeq,
SwissProt/PIR/GeneSeq, JICST (JOIS), MEDLINE (STN)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO, 01/00824, A (Protegene Inc.), 04 January, 2001 (04.01.01), & AU 200052499 A	1-11, 16-18, 24-26, 28-31
X	WO, 00/11942, A (Gene Logic Inc.), 09 March, 2000 (09.03.00), & AU 9957989 A	1-11, 16-18, 24-26, 28-31
X	WO, 00/61755, A (Chiron Corp.), 19 October, 2000 (19.10.00), & EP 1177287 A2 & AU 200043381 A	1-11, 16-18, 24-26, 28-31
X	WO, 00/56889, A2 (Genentech Inc.), 28 September, 2000 (28.09.00), & AU 200038648 A & EP 1169442 A2	1-11, 16-18, 24-26, 28-31

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search
22 March, 2002 (22.03.02)

Date of mailing of the international search report
09 April, 2002 (09.04.02)

Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP01/11389

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 12, 20, 23
because they relate to subject matter not required to be searched by this Authority, namely:
Claims 12, 20 and 23 pertain to diagnostic methods to be practiced on the human body and methods for treatment of the human body by therapy.
2. ☒ Claims Nos.: 19, 21, 22
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
(See extra sheet)
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)This International Searching Authority found multiple inventions in this international application, as follows:
(see extra sheet)

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP01/11389

Continuation of A. CLASSIFICATION OF SUBJECT MATTER (International Patent Classification (IPC))

Int.Cl⁷ C12N15/12, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, A61K31/7088, A61K38/02, A61K39/395, A61K45/00, A61K48/00, A61P29/00, A61P35/00, A61P37/00, C12Q1/68, C12N9/00, G01N33/15, G01N33/50, G01N33/53, G01N33/577, G01N33/68
(According to International Patent Classification (IPC) or to both national classification and IPC)

Continuation of B. FIELDS SEARCHED

Minimum Documentation Searched (International Patent Classification (IPC))

Int.Cl⁷ C12N15/12, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, A61K31/7088, A61K38/02, A61K39/395, A61K45/00, A61K48/00, A61P29/00, A61P35/00, A61P37/00, C12Q1/68, C12N9/00, G01N33/15, G01N33/50, G01N33/53, G01N33/577, G01N33/68
Minimum documentation searched (classification system followed by classification symbols)

Continuation of Box No. I (2) of Continuation of first sheet (1)

Concerning the "ribozyme inhibiting the activation of NF- κ B by the cleavage of RNA encoding the protein as set forth in claim 7" described in claim 19, the "medicinal composition produced by the method as set forth in claim 14 as inhibiting the activation of NF- κ B or activating" as described in claim 21, and the "medicinal composition as set forth in claim 21" as described in claim 22, it is completely unknown what specific compounds are involved in the scopes thereof and what are not. Thus, these claims are described in an extremely unclear manner.

Continuation of Box No. II of Continuation of first sheet (1)

In the inventions as set forth in claims 1 to 11, 16 to 18, 24 to 26 and 28 to 31, the amino acid sequences represented respectively by SEQ ID NOS:1, 3, 5, 7, 9, 11, - - - 174, 176, 178 and 180 have no chemical structure in common but exhibit a common function of encoding a protein having an effect of activating NF- κ B.

However, document 1 (JP 11-155581 A (Okamoto Hisashi) 1999.06.15) discloses the amino acid sequence of a novel protein participating in the regulation of NF- κ B signal activity, a DNA sequence encoded by the protein, a transformant having this DNA, an antibody against the above novel protein and an antisense to the DNA; document 2 (Li X, et al., Proc. Natl. Acad. Sci. U.S.A. (2000 Sep), Vol. 97, No. 19, p. 10489-10493) discloses a novel protein Act1 activating NF- κ B; and document 3 (Srinvasula SM, et. al., J. Biol. Chem. (1999), Vol. 274, No. 25, p. 17946-17954) discloses a novel protein CLAP activating NF- κ B. Therefore, the common matter as described above falls within the category of the prior arts and thus it is not considered that the "protein having an effect of activating NF- κ B" is a special technical feature in the meaning as defined in PCT Rule 13.2.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP01/11389

Such being the case, 90 proteins having the amino acid sequences respectively represented by SEQ ID NOS:1, 3, 5, 7, 9, 11, - - - 174, 176, 178 and 180 are not considered as relating to a group of inventions so linked as to form a single general inventive concept but to constitute groups of inventions consisting of 90 inventions respectively relating to 90 proteins different from each other.

Concerning the "method of screening a compound with respect to the NF- κ B activation inhibition activity or the promotion activity" of the inventions as set forth in claims 13 to 15, the above-described common matter "protein having an effect of activating NF- κ B" falls within the category of the prior art and thus cannot be regarded as a special technical feature in the meaning as defined in PCT Rule 13.2. Thus, it cannot be considered as relating to a group of inventions so linked as to form a single general inventive concept but constitute the 91st group of inventions.

Because of having no special technical feature as described above, furthermore, claim 27 constitutes the 92nd group of inventions.

Such being the case, there is no special technical matter common to all of the claims and thus these two groups of inventions are not considered as relating to a group of inventions so linked as to form a single general inventive concept.

Accordingly, it is recognized that the following 92 groups of inventions are described in the claims:

(1) in claims 1 to 11, 16 to 18, 24 to 26 and 28 to 31, the parts concerning SEQ ID NO:1;

(2) in claims 1 to 11, 16 to 18, 24 to 26 and 28 to 31, the parts concerning SEQ ID NO:3;

(3) in claims 1 to 11, 16 to 18, 24 to 26 and 28 to 31, the parts concerning SEQ ID NO:5;

:

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(89) in claims 1 to 11, 16 to 18, 24 to 26 and 28 to 31, the parts concerning SEQ ID NO:178;

(90) in claims 1 to 11, 16 to 18, 24 to 26 and 28 to 31, the parts concerning SEQ ID NO:180;

(91) in claims 13 to 15, the parts concerning the method of screening a compound with respect to the NF- κ B activation inhibition activity or the promotion activity"; and

(92) the part concerning the method of acquiring a novel full-length cDNA having the function as described in claim 27.

In claims 1 to 11, 16 to 18, 24 to 26 and 28 to 31, the parts relating to SEQ ID NO:1

国際調査報告

国際出願番号 PCT/JPO1/11389

A. 発明の属する分野の分類 (国際特許分類 (IPC)) Int. Cl ¹ C12N15/12, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, A61K31/7088, A61K38/02, A61K39/395, A61K45/00, A61K48/00, A61P29/00, A61P35/00, A61P37/00, C12Q1/68, C12N9/00, G01N33/15, G01N33/50, G01N33/53, G01N33/577, G01N33/68		
B. 調査を行った分野 調査を行った最小限資料 (国際特許分類 (IPC)) Int. Cl ¹ C12N15/12, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, A61K31/7088, A61K38/02, A61K39/395, A61K45/00, A61K48/00, A61P29/00, A61P35/00, A61P37/00, C12Q1/68, C12N9/00, G01N33/15, G01N33/50, G01N33/53, G01N33/577, G01N33/68		
最小限資料以外の資料で調査を行った分野に含まれるもの		
国際調査で利用した電子データベース (データベースの名称、調査に使用した用語) Genebank/EMBL/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq, JICST (JOIS), MEDLINE (STN)		
C. 関連すると認められる文献		
引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
P X	WO 01/00824 A (PROTEGENE INC) 2001. 01. 04 & AU 200052499 A	1-11, 16-18, 24-26, 28-31
X	WO 00/11942 A (GENE LOGIC INC) 2000. 03. 09 & AU 9957989 A	1-11, 16-18, 24-26, 28-31
X	WO 00/61755 A (CHIRON CORPORATION) 2000. 10. 19 & EP 1177287 A2 & AU 200043381 A	1-11, 16-18, 24-26, 28-31
<input checked="" type="checkbox"/> C欄の続きにも文献が列挙されている。 <input type="checkbox"/> パテントファミリーに関する別紙を参照。		
* 引用文献のカテゴリー 「A」 特に関連のある文献ではなく、一般的な技術水準を示すもの 「E」 国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの 「L」 優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献 (理由を付す) 「O」 口頭による開示、使用、展示等に言及する文献 「P」 国際出願日前で、かつ優先権の主張の基礎となる出願日の後に公表された文献 「T」 国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの 「X」 特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの 「Y」 特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの 「&」 同一パテントファミリー文献		
国際調査を完了した日 22. 03. 02	国際調査報告の発送日 09.04.02	
国際調査機関の名称及びあて先 日本国特許庁 (ISA/J P) 郵便番号100-8915 東京都千代田区霞が関三丁目4番3号	特許庁審査官 (権限のある職員) 新見 浩一 電話番号 03-3581-1101 内線 3488	4N 9839

C (続き) . 関連すると認められる文献		
引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
X	WO 00/56889 A2 (GENENTECH INC) 2000. 09. 28 & AU 200038648 A & EP 1169442 A2	1-11, 16-18, 24-26, 28-31

第I欄 請求の範囲の一部の調査ができないときの意見 (第1ページの2の続き)

法第8条第3項 (PCT17条(2)(a))の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. ☒ 請求の範囲 12, 20, 23 は、この国際調査機関が調査をすることを要しない対象に係るものである。
つまり、
請求の範囲12, 20, 23は、人体の診断方法、ヒトの身体の治療による処置方法に該当するものである。
2. ☒ 請求の範囲 19, 21, 22 は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、
請求の範囲19に記載の「・・または7記載のタンパク質をコードするRNAの開裂により、NF- κ Bの活性化を阻害するリボザイム」、請求の範囲21の「NF- κ Bの活性化を阻害または活性化するものとして請求項14に記載の方法により製造された医薬組成物」、請求の範囲22の「・・請求項21記載の医薬組成物」については、化合物として具体的にどの化合物が含まれ、どのような化合物が含まれないのかが全く不明であって、請求の範囲の記載は著しく不明確である。
3. ☐ 請求の範囲 ・・ は、従属請求の範囲であってPCT規則6.4(a)の第2文及び第3文の規定に従って記載されていない。

第II欄 発明の単一性が欠如しているときの意見 (第1ページの3の続き)

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

別紙 (特別頁参照)

1. ☐ 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。
2. ☐ 追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。
3. ☐ 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったため、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。
4. ☒ 出願人が必要な追加調査手数料を期間内に納付しなかったため、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。
請求の範囲1-11, 16-18, 24-26, 28-31のうち、配列番号1に関する部分

追加調査手数料の異議の申立てに関する注意

- ☐ 追加調査手数料の納付と共に出願人から異議申立てがあった。
☐ 追加調査手数料の納付と共に出願人から異議申立てがなかった。

請求の範囲1-11, 16-18, 24-26, 28-31に係る発明の、配列番号1, 3, 5, 7, 9, 11, . . . , 174, 176, 178または180のいずれかで表されるアミノ酸配列は、共通の化学構造を有するものでもなく、NF κ Bを活性化する作用を有するタンパク質をコードすることにおいてのみ共通するものである。

しかしながら、文献1 (JP 11-155581 A(岡本 尚)1999.06.15) には、NF κ Bシグナルの活性制御に関わる新規蛋白質のアミノ酸配列、該蛋白質がコードするDNA配列、該DNAを有する形質転換体、該新規蛋白質に対する抗体、該DNAに対するアンチセンスについて、文献2 (Li X, et. al., Proc. Natl. Acad. Sci. U.S.A. (2000 Sep), Vol. 97, No. 19, p. 10489-10493) には、NF- κ Bを活性化させる新規蛋白質Act1について、文献3 (Srinivasula SM, et. al., J. Biol. Chem. (1999), Vol. 274, No. 25, p. 17946-17954) には、NF- κ Bを活性化させる新規蛋白質CLAPについて記載されていることから、上記共通事項は先行技術の域をでるものではなく、「NF κ Bを活性化する作用を有するタンパク質」はPCT規則13.2における特別な技術的特徴であるとはいえない。

よって、配列番号1, 3, 5, 7, 9, 11, . . . , 174, 176, 178または180のいずれかで表されるアミノ酸配列からなる90個の蛋白質は、単一の一般的発明概念を形成するように関連している一群の発明群であるとはいえず、異なった90個の蛋白質それぞれに関する90個の発明からなる発明群であると認める。

また、請求の範囲13-15に係る発明の「NF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングする方法」についても、上記共通事項である「NF κ Bを活性化する作用を有するタンパク質」が先行技術の域を出るものではなく、PCT規則13.2における特別な技術特徴であるとは言えない以上、上記90個の発明群と単一の一般的発明概念を形成するように連関している一群の発明と認められないことから、第91の発明群を構成すると認める。

さらに、請求の範囲27は、上記特別な技術的特徴を有さず、第92の発明群を構成する。

それ故に請求の範囲の全てに共通の特別な技術事項はなく、上記発明群が単一の一般的な発明概念を形成するように連関している一群の発明であるとは認められない。

すなわち、請求の範囲には、

- (1) 請求の範囲1-11, 16-18, 24-26, 28-31のうち、配列番号1に関する部分
- (2) 請求の範囲1-11, 16-18, 24-26, 28-31のうち、配列番号3に関する部分
- (3) 請求の範囲1-11, 16-18, 24-26, 28-31のうち、配列番号5に関する部分

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- (89) 請求の範囲1-11, 16-18, 24-26, 28-31のうち、配列番号178に関する部分
- (90) 請求の範囲1-11, 16-18, 24-26, 28-31のうち、配列番号180に関する部分
- (91) 請求の範囲13-15の NF- κ B活性化の阻害活性または促進活性について化合物をスクリーニングする方法に関する部分
- (92) 請求の範囲27の機能をもつ新規完全長cDNAの取得方法に関する部分

の第92発明が記載されていると認められる。